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Maximum DB
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Maximum Match 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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seq length: 2000000000
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1: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*

2: /cgn2_6/ptodata/2/pubpaa/US01_NEW_PUB.pep:*

3: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*

4: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*

5: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*

6: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*

7: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*

8: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
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Gapop 10.0 , Gapext 0.5
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                                             Maximum Match 100%
Listing first 45 summaries
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Copyright (c) 1993 - 2005 Compugen Ltd.
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                    US-10-131-826A-412
US-10-793-626-746
US-10-821-234-915
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US-10-821-234-915
US-10-821-234-915
US-10-93-626-3112
US-10-793-626-3236
US-11-074-176-38
US-11-074-176-38
US-11-074-176-38
US-11-074-176-38
US-11-057-058-62
US-11-057-626-1990
US-11-057-626-1990
US-11-057-626-190
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(without alignments)
12.124 Million cell updates/sec
Sequence 412, App
Sequence 66, Appl
Sequence 746, App
Sequence 915, App
Sequence 915, App
Sequence 98, App1
Sequence 3112, Ap
Sequence 3114, Ap
Sequence 316, App
Sequence 306, App
Sequence 306, App
Sequence 318, App
Sequence 31, App
Sequence 211, App
Sequence 10, Appl
Sequence 112, Ap
Sequence 112, Ap
Sequence 190, Ap
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7 US-11-096-051-10	7 US-11-096-051-2	7 US-11-096-051-4	7 US-11-096-051-20	7 US-11-096-051-6	7 US-11-096-051-14	1 US-10-821-234-914	7 US-11-077-550-141	1 US-10-131-826A-234	1 US-10-821-234-1147	7 US-11-082-389-86	1 US-10-793-626-2220	7 US-11-082-389-334	1 US-10-131-826A-82	7 US-11-012-762-74	7 US-11-060-008-11	1 US-10-821-234-1623	1 US-10-821-234-1563	1 US-10-821-234-1199	1 US-10-821-234-1443
Sequence 10, Appi	•	Sequence 4, Appli	Sequence 20, Appl	Sequence 6, Appli	Sequence 14, Appl		•	Sequence 234, App	``	Sequence 86, Appl	Sequence 2220, Ap	Sequence 334, App	-	•	Sequence 11, Appl	23	•	•	Sequence 1443, Ap

APPLICANY: CROCK, CARRIED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3330R1C128 CURRENT APPLICATION NUMBER: US/10/131,826A CURRENT FILING DATE: 2002-04-24 PRIOR APPLICATION NUMBER: 60/049911 PRIOR FILLING DATE: 1997-06-18 PRIOR APPLICATION NUMBER: 60/05974 PRIOR FILING DATE: 1997-09-17 PRIOR APPLICATION NUMBER: 60/059113 PRIOR APPLICATION NUMBER: 60/059115 PRIOR APPLICATION NUMBER: 60/059117 PRIOR APPLICATION NUMBER: 60/059117 PRIOR APPLICATION NUMBER: 60/059117 PRIOR APPLICATION NUMBER: 60/059122 PRIOR PILING DATE: 1997-09-17 PRIOR APPLICATION NUMBER: 60/059122 PRIOR PILING DATE: 1997-09-17 PRIOR APPLICATION NUMBER: 60/059124 PRIOR APPLICATION NUMBER: 60/059125 PRIOR APPLICATION NUMBER: 60/059184 PRIOR APPLICATION NUMBER: 60/059184 PRIOR APPLICATION NUMBER: 60/059352 PRIOR FILING DATE: 1997-09-18 PRIOR FILING DATE: 1997-09-18 PRIOR APPLICATION NUMBER: 60/059352 RESULT 1 US-10-131-826A-412 Publication No. GENERAL INFORMATION: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: Baker, Kevin P. APPLICANT: Beresini, Maur APPLICANT: APPLICANT: APPLICANT: PRIOR FILING DATE: 1997-09-19 PRIOR APPLICATION NUMBER: 60/059588 PRIOR FILING DATE: 1997-09-19 APPLICANT: APPLICANT: APPLICANT: APPLICANT: Watanabe, Colin K Wood, William Stewart, Timothy A. Tumas, Daniel Smith, Victoria Sherwood, Steven Godowski, Paul J. Gurney, Austin L. Goddard, Audrey Gerritsen, Mary E. Gao, Wei-Qiang Filvaroff, Ellen Desnoyers, Luc DeForge, Laura Beresini,Maureen Application US/10131826A US20050245730A1

Prior Application data removed - See File Wrapper or PALM

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Sequence 66, Application US/10793626

Publication No. US20050255478A1

GENERAL INFORMATION:

APPLICANT: KIMMERLY, WILLIAM JOHN
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERWIDIS NUCLEIC ACIDS AND
FILE REFERENCE: PU3480US
CURRENT APPLICATION NUMBER: US/10/793,626

GURRENT FILING DATE: 2004-03-04

PRIOR APPLICATION NUMBER: 60/164,258

PRIOR APPLICATION NUMBER: 60/164,258

PRIOR FILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 66
                                                                                            FILE REFERENCE: PU3480US
CURRENT APPLICATION NUMBER: US/10/793,626
CURRENT FILING DATE: 2004-03-04
PRIOR APPLICATION NUMBER: 60/164,258
PRIOR FILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 746
LENGTH: 297
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE: THEODEMARTION: Description of Artificial
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OTHER INFORMATION: Description of Artificial Sequence: synthetic

OTHER INFORMATION: amino acid sequence

US-10-793-626-66
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; ORGANISM: Homo Sapien
US-10-131-826A-412
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Best Local Similarity
Thes 7; Conserv
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APPLICANT: KIMMERLY, WILLIAM JOHN
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
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SEQ ID NO 412
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                       Sequence 746, Appropriate Publication No.
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ORGANISM: Artificial Sequence
                                                                  OTHER INFORMATION: Description of Artificial Sequence: synthetic OTHER INFORMATION: amino acid sequence
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Pred. No. 22;
1; Mismatches
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Score 33;
Pred. No.
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Pred. No. 14;
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DB
14;
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              Length 297;
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FILE REFERENCE: 821A
CURRENT APPLICATION NUMBER: US/10/821,234
CURRENT FILING DATE: 2004-04-07
PRIOR APPLICATION NUMBER: US 60/462,047
PRIOR FILING DATE: 2003-04-07
PRIOR FILING DATE: 2004-04-07
PRIOR FILING DATE: 2003-04-07
PRIOR FILING DATE: 20
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; NAME/KEY: misc feature
; LOCATION: (1)...(169)
; OTHER INFORMATION: Xaa = any amino acid or nothing
US-10-821-234-1234
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US-10-821-234-915
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                                                                                                                                                                                                                                                                             SOFTWARE: pt_SEQ_genes Version 1.0
SEQ ID NO 915
LENGTH: 478
TYPE: PRT
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Publication No. US20050255114A1
GENERAL INFORMATION:
                                                                     Best Local Similarity
Matches 5; Conserv
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CURRENT FILING DATE: 2004-04-07
PRIOR APPLICATION NUMBER: US 60/462,047
PRIOR FILING DATE: 2003-04-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Labat, Ivan
APPLICANT: Stache-Crain, Birgit
APPLICANT: Andarmani, Susan
APPLICANT: Tang, Y. Tom
TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
FILE REFERENCE: 821A
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APPLICANT: Tang, Y. Tom
TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
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APPLICANT: Stache-Crain, Birgit
                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 1704
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          KKRYDREFL 9
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                                                                                Conservative
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                                                                                                            Score 32;
Pred. No.
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Pred. No. 12;
                                                                                   Mismatches
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                                                                                                                                           Length 478;
                                                                                Indels
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APPLICANT: Klaenhammer, Todd R.
APPLICANT: Russell, William M.
APPLICANT: Altermann, Eric
APPLICANT: Altermann, Eric
APPLICANT: McAuliffe, Olivia
APPLICANT: Nucleic Acid Sequences Encoding
TITLE OF INVENTION: Stress-Related Proteins and Uses
TITLE OF INVENTION: Stress-Related Proteins and Uses
FILE REFERENCE: 5051-694
CURRENT APPLICATION NUMBER: US/11/074,176
CURRENT APPLICATION NUMBER: 2005-03-07
PRIOR APPLICATION NUMBER: 60/551,161
PRIOR APPLICATION NUMBER: 60/551,161
PRIOR APPLICATION NUMBER: 60/551,161
PRIOR APPLICATION NUMBER: 60/551,161
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US-11-074-176-98
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                                                                                                                   US-10-793-626-3184
                                                                                                                                                        RESULT 8
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OTHER INFORMATION: Description of Artificial Sequence: synthetic;
OTHER INFORMATION: amino acid sequence
US-10-793-626-3112
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TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REFERENCE: PU3480US
CURRENT APPLICATION NUMBER: US/10/793,626
CURRENT FILING DATE: 2004-03-04
PRIOR APPLICATION NUMBER: 60/164,258
PRIOR FILING DATE: 1999-11-09
PR
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SEQ ID NO 98
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 3112, Application US/10793626 Publication No. US20050255478A1 GENERAL INFORMATION:
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Sequence 3184, Application US/10793626 Publication No. US20050255478A1 GENERAL INFORMATION:
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Best Local (
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TYPE: PRT
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nes 7; Conserv
                                                                                                                                                                                                                                                                           118 KRHKQTFLLG 127
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Similarity 60.0%;
6; Conservative
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; Pred. No. 33;
2; Mismatches
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US-10-793-626-3236
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Best Local S
Matches 5
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NUMBER OF SEQ ID NOS: 117
SOFTWARE: FABESEQ for Windows Version 4.0
SEQ ID NO 41
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Sequence 3236, Application US/10793626
Publication No. US20050255478A1
GENERAL INFORMATION:
APPLICANT: KIMMERLY, WILLIAM JOHN
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REFERENCE: PUJ480US
CURRENT APPLICATION NUMBER: US/10/793,626
CURRENT APPLICATION NUMBER: 00/164,258
PRIOR APPLICATION NUMBER: 60/164,258
PRIOR FILING DATE: 1999-11-09
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CURRENT FILING DATE: 2004-03-04
PRIOR APPLICATION NUMBER: 60/164,258
PRIOR FILING DATE: 1999-11-09
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CURRENT APPLICATION NUMBER: US/10/981,873
CURRENT FILING DATE: 2004-11-05
PRIOR APPLICATION NUMBER: US 60/517,848
PRIOR FILING DATE: 2003-11-05
PRIOR APPLICATION NUMBER: US 60/591,548
PRIOR APPLICATION NUMBER: US 60/591,548
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TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REFERENCE: PU3480US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Verdine, Gregory
TITLE OF INVENTION: STABILIZED ALPHA HELICAL PEPTIDES AND
TITLE OF INVENTION: USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Walensky, Loren D.
APPLICANT: Korsmeyer, Stanley J.
APPLICANT: Verdine, Gregory
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ORGANISM: Artificial Sequence
FEATURE:
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71.4%;
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Sequence 18, Application US/11074176
Publication No. US20050250135A1
GENERAL INFORMATION:
APPLICANT: Klaenhammer, Todd R.
APPLICANT: Russell, William M.
APPLICANT: McAuliffe, Olivia
APPLICANT: McAuliffe, Olivia
APPLICANT: McAuliffe, Olivia
APPLICANT: Peril, Andrea Azcarate
ITILE OF INVENTION: Nucleic Acid Sequences Encoding
ITILE OF INVENTION: Stress-Related Proteins and Uses Therefore
ITILE REFERENCE: 5051-694
CURRENT APPLICATION NUMBER: US/11/074,176
CURRENT APPLICATION NUMBER: 00/551,161
PRIOR APPLICATION NUMBER: 60/551,161
PRIOR APPLICATION NUMBER: 5095-03-07
PRIOR APPLICATION NUMBER: 5095-03-07
PRIOR APPLICATION NUMBER: 5095-1,161
PRIOR FILING DATE: 2004-03-08
NUMBER OF SEQ ID NOS: 381
SOFTWARE: FastSEQ for Windows Version 4.0
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US-11-074-176-306
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TITLE OF INVENTION: Stress-Related Proteins and Uses Therefore
FILE REFERENCE: 501-694
CURRENT APPLICATION NUMBER: US/11/074,176
CURRENT FILING DATE: 2005-03-07
PRIOR APPLICATION NUMBER: 60/551,161
PRIOR FILING DATE: 2004-03-08
NUMBER OF SEQ ID NOS: 381
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 306
LENGTH: 718
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SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3236
LENGTH: 411
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Best Local (
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APPLICANT: Russell, William M.
APPLICANT: Altermann, Eric
APPLICANT: WcAuliffe, Olivia
APPLICANT: Peril, Andrea Azcarate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE: OTHER INFORMATION: Description of Artificial Sequence: synthetic OTHER INFORMATION: amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Lactobacillus acidophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
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nes 5; Conservarion
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Local Similarity 75.0%;
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Pred. No. 64;
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Pred. No. 1.1e+02;
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                  Query Match
Best Local Similarity
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Sequence 62, Application US/11057058
Publication No. US20050244400A1
GENERAL INFORMATION:
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                                                                                                         US-11-057-058-62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: KIMMERLY, WILLIAM JOHN
TITLE OF INVENTION: STAFHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REFERENCE: PU3480US
CURRENT APPLICATION NUMBER: US/10/793,626
CURRENT FILING DATE: 2004-03-04
PRIOR APPLICATION UNMBER: 60/164,258
PRIOR APPLICATION UNMBER: 60/164,258
PRIOR FILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 3324
LENGTH: 944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 3324, Application US/10793626 Publication No. US20050255478A1 GENERAL INFORMATION:
                                                                                                                                                                               SOFTWARE: PatentIn version 3.3 SEQ ID NO 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 18
LENGTH: 723
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Best Local Similarity
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Best Local Similarity
Matches 5; Conserv
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TITLE OF INVENTION: ACID ALPHA-GLUCOSIDASE AND FRAGMENTS THEREOF
FILE REFERENCE: SYM-011
CURRENT APPLICATION NUMBER: US/11/057,058
CURRENT FILING DATE: 2005-02-10
CURRENT FILING DATE: 2005-02-10
                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: US 60/543,812
PRIOR FILING DATE: 2004-02-10
NUMBER OF SEQ ID NOS: 68
                                                                                                                                                                                                                                                                                                                                                APPLICANT: LeBowitz, Jonathan APPLICANT: Maga, John
                                                                                                                                             LENGTH: 1827
TYPE: PRT
                                                                                                                            ORGANISM: Rabbit sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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85.7%;
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Pred. No. 1.4e+02;
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Pred. No. 1.1e+02
                                                    Score 30; DB 7;
Pred. No. 2.6e+02;
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                                                                     Length 1827;
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RESULT 15

US-10-821-234-916

US-10-821-234-916

Sequence 916, Application US/10821234

Publication No. US20050255114A1

GENERAL INFORMATION:

APPLICANT: Labar, Itan

APPLICANT: Labar, Itan

APPLICANT: Tang, Y. Tom

APPLICANT: Tang, Y. Tom

APPLICANT: Tang, Y. Tom

ITILE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia

FILE REFERENCE: 821A

CURRENT FILING DATE: 2004-04-07

PRIOR APPLICATION NUMBER: US 60/462,047

PRIOR PRIVALE: US
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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seq length: 2000000000
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Gapop 10.0 , Gapext 0.5
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64
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KKRYDREFLLGF 12
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Copyright (c) 1993 - 2005 Compugen Ltd.
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2872
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1473
142
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1449
      US-09-973-473-9

US-09-973-473-11

US-09-973-473-11

US-09-973-473-10

US-10-450-763-50799

US-10-335-977-6279

US-10-335-977-6270

US-10-335-977-6270

US-10-437-963-114937

US-10-425-115-282367

US-10-437-963-1187843

US-10-437-963-1187843

US-10-435-115-282687

US-10-425-115-282687

US-10-501-282-4468

US-10-437-963-169968

US-10-425-115-35791

US-10-425-115-357901

US-10-425-115-357998
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                                                                                                                                                                                   Sequence 9, Appli
Sequence 11, Appl
Sequence 10, Appl
Sequence 50799, A
Sequence 62703, Ap
Sequence 6269, Ap
Sequence 6270, Ap
Sequence 6271, Ap
Sequence 114937,
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312, App
282367,
1167843,
69, Appl
116, Appl
288687,
1154949,
1154949,
4466, Ap
4466, Ap
4466, Ap
4968, Ap
4954, A
357721, A
357721, A
3577898,
322315, A
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4 5	44	43	42	41	40	39	38	37	36	35	34	ယ္သ	32	31	30	29	28
37	37	37	37	37	37	37	37	37	37	37	37	37	37	37	37	37	37
57.8	57.8	57.8	57.8	57.8	57.8	57.8	57.8	57.8	57.8	57.8	57.8	57.8	57.8	•	•	57.8	57.8
670	570	521	381	267	267	267	267	267	267	267	267	267	267	267	211	192	76
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US-09-833-245-1304	US-10-282-122A-65941	•	US-10-767-701-36815	US-10-138-898-106	US-10-405-660-106	US-10-400-902-24	US-10-139-218-106	US-10-139-296-106	US-10-138-916-106	US-10-138-905-106	US-10-139-031-106	US-10-138-838-106	US-09-976-800-106	US-09-911-781-24	US-10-425-115-328208	US-10-437-963-154057	US-10-767-701-51018
Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence		Sequence
1304, Ap	-	43422, A	36815, A	106, App	•	-		106, App	-		•	•	106, App	*		154057,	51018, A

APPLICANT: SONENBERG, Nahum APPLICANT: TREMBLAY, MICHAI APPLICANT: TREMBLAY, MICHAI APPLICANT: TSUKIAYAMA-KOHARA, KYOKO TITLE OF INVENTION: NON-HUMAN TRANSGENIC ANIMP TITLE OF INVENTION: SOMATIC CELLS CONTAIN A F TITLE OF INVENTION: ENCODING 4E-BP1 FILE REFERENCE: 51401200400 CURRENT APPLICATION NUMBER: US/09/973,473 CURRENT APPLICATION NUMBER: US/09/973,473 CURRENT FILING DATE: 2001-0-03 PRIOR APPLICATION NUMBER: 6C/7CA00/00388 PRIOR APPLICATION NUMBER: 6C/128,559 PRIOR APPLICATION NUMBER: 60/128,559 PRIOR APPLICATION NUMBER: 60/179,743 US-09-973-473-11 ; Sequence 11, Application US/09973473 ; Publication No. US20030041341A1 ; ORGANISM: Homo sapiens US-09-973-473-9 US-09-973-473-9 밁 RESULT 2 GENERAL INFORMATION: APPLICANT: SONENBERG, Nahum APPLICANT: TREMBLAY, Michel APPLICANT: TREMBLAY, Michel APPLICANT: TSUKIAYAMA-KOHARA, KYOKO TITLE OF INVENTION: NON-HUMAN TRANSGENIC ANIMAL WHOSE GERM CELLS AND TITLE OF INVENTION: SOMATIC CELLS CONTAIN A KNOCKOUT MUTATION IN DNA TITLE OF INVENTION: ENCODING 4E-BP1 FILE REFERENCE: 514012000400 Sequence 9, Application US/09973473 Publication No. US20030041341A1 GENERAL INFORMATION: Query Match Best Local S Matches LENGTH: 16 TYPE: PRT CURRENT APPLICATION NUMBER: US/09/973,473 12; 16 1 KKRYDREFLLGF 12 Similarity KKRYDREFLLGF 12 100.0%; ilarity 100.0%; Conservative 0 0, Score 64; DB 3; Pred. No. 9.7e-05;); Mismatches 0; ANIMAL WHOSE Length 16 Indels GERM CELLS AND MUTATION IN DNA 0; Gaps

CURRENT FILING DATE:

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RESULT 4

US-10-450-763-50799
US-10-450-763-50799, Application US/10450763
; Sequence 50799, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT APPLICATION NUMBER: PCT/US01/08631
; PRIOR APPLICATION NUMBER: PCT/US01/08631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: SOMENBERG, Nahum
APPLICANT: TREMBLAY, Michel
APPLICANT: TREMBLAY, Michel
APPLICANT: TREMBLAY, Michel
APPLICANT: TSUKIAYAMA-KOHARA, KYOKO
TITLE OF INVENTION: NON-HUMAN TRANSGENIC ANIMAL WHOSE GERM CELLS AND
TITLE OF INVENTION: SOMATIC CELLS CONTAIN A KNOCKOUT MUTATION IN DNA
TITLE OF INVENTION: ENCODING 4E-BP1
FILE REFERENCE: 514012000400
CURRENT APPLICATION NUMBER: US/09/973,473
CURRENT PILING DATE: 2001-10-03
PRIOR APPLICATION NUMBER: FCT/CANO/00388
PRIOR APPLICATION NUMBER: 60/179,743
PRIOR FILING DATE: 1999-04-09
PRIOR FILING DATE: 2000-02-02
NUMBER OF SEQ ID NOS: 27
SOPTWARE: Patentin Ver. 2.1
SEQ ID NO 10
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PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: 60/128,559
PRIOR FILING DATE: 1999-04-09
PRIOR APPLICATION NUMBER: 60/179,743
PRIOR APPLICATION NUMBER: 60/179,743
PRIOR FILING DATE: 2000-02-02
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 11
LENGTH: 16
TYPE: PRT
ORGANISM: Danio rerio
US-09-973-473-11
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-973-473-10
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US-09-973-473-10
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Best Local Similarity 83.3%;
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Pred. No. 0.01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 64; DB 3;
Pred. No. 9.7e-05;
                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 16;
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PRIOR APPLICATION NUMBER: 09/540,217
PRIOR FILLING DATE: 2000-03-31
PRIOR PELLOATION NUMBER: 09/649,167
PRIOR FILLING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 60736
SOFTWARE: Custom
SEQ ID NO 50799
LENGTH: 1756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; LOCATION: (1)...(1756)
; OTHER INFORMATION: Xaa = X or * as defined in Table US-10-450-763-50799
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 9703, Application US/10335977
Publication No. US20040052799A1
GENERAL INFORMATION:
APPLICANT: DOUGLAS SMITH et al
APPLICANT: DOUGLAS SMITH et al
TITLE OF INVENTION: NUCLEIC ACID AMINO ACID SEQUENCES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 82.8%;
Best Local Similarity 83.3%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE: DOMAIN
NAME/KEY: DOMAIN
LOCATION: (49)..(59)
OTHER INFORMATION: TYPE I ANTIFREEZE PROTEIN SIGNATURE domain identified by
OTHER INFORMATION: eMATRIX, accession number PR00308C, p-value=8.013e-09, ro
OTHER INFORMATION: 3.83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: DOMAIN
LOCATION: (1689)..(1756)
OTHER INFORMATION: eIF4-gamma/eIF5/eIF2-epsilon domain identified by PFam,
OTHER INFORMATION: accession name IF5_eIF4_eIF2, E-value=0.0038, PFam score of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc_feature LOCATION: (1)...(1756)
                    TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 9703:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Homo sapiens
                                                                                 COMPUTER: IBM PC Compatible
OPERATING SYSTEM: WINDOWS NT 4.0
SOFTWARE: UNIX
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/10/335,977
FILING DATE: 30-Dec-2002
PRIOR APPLICATION UNMBER: 08/993,002
PRIOR APPLICATION UNMBER: 08/993,002
PRIOR TILING DATE: 17-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION UNMBER: 36,207
REFERENCE/DOCKET NUMBER: GIN-018
TELECOMMUNICATION INFORMATION:
TELECOMOUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 10031
CORRESPONDENCE ADDRESS:
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               790 KKOYDREFLLDF 801
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET:
                                                                    TELEPHONE: (617)227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: LAHIVE & COCKFIELD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28 State Street
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 53;
Pred. No. 1
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NAME/KEY: misc feature LOCATION: (B) LOCATION 1...226 SEQUENCE DESCRIPTION: SEQ ID NO: 9703: US-10-335-977-9703
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                                            US-10-335-977-6269
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Sequence 6269, Application US/10335977

Publication No. US20040052799A1

GENERAL INFORMATION:

APPLICANT: DOUGLAS SMITH et al

APPLICANT: DOUGLAS SMITH ET AMINO ACID SEQUENCES

RELATING TO HELICOBACTER PYLORI FOR

BURNESSES DOUGLASS: 10031

CORRESPONDENCE ADDRESS:

ADDRESSEE: LAHIVE & COCKFIELD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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Query Match
                                                                                                                                                                                                                                                                                                                       TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 6269:
                                                                                                                                                                                                                                                                                                                                                                                    PRILING DATE: 30-Dec-2002

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/993,002

FILING DATE: 17-DEC-1997

ATTORNEY/AGENT INFORMATION:
NAME: Mandaragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: GTN-018
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM IS09660
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: Windows NT 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORIGINAL SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: UNIX
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/335,977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
                                                              NAME/KEY: misc_feature
LOCATION: (B) LOCATION 1...339
SEQUENCE DESCRIPTION: SEQ ID NO: 620
                                                                                                                             FEATURE:
                                                                                                                                                                        MOLECULE TYPE: protein HYPOTHETICAL: YES ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        129 KKRYEKEFNLLWVGLLGF 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           l Similarity
10; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Helicobacter pylori
                                                                                                                                                                                                                                  LENGTH: 339 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 02109-1875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: Massachusetts
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 28 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 226 amino acids
                                                                                                                                                    ORGANISM: Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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    68.8%;
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Pred. No. 7
    Score 44; DB 4;
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                                                                 6269:
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  Length 339;
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                                          RESULT 8
US-10-335-977-6271
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LOCATION: (B) LOCATION 1...553
SEQUENCE DESCRIPTION: SEQ ID NO: 6270:
US-10-335-977-6270
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US-10-335-977-6270
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Publication No. US20040052799A1

PUBLICANTION: GENERAL INFORMATION:

APPLICANT: DOUGLAS SMITH et al

APPLICANT: DOUGLAS SMITH et al

APPLICANT: MUCLEIC ACID AND AMINO ACID SEQUENCES

RELATING TO HELICOBACTER PYLORI FOR

DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: GTN-018
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEPHONE: (617)742-4214
INFORMATION FOR SEQ ID NO: 6270:
SEQUENCE CHARACTERISTICS:
LENGTH: 553 amino acids
TYPE: amino acid
Sequence 6271, Application US/10335977 Publication No. US20040052799A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity Matches 10; Conserv
                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                    Query Match
Best Local Similarity
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APPLICATION NUMBER: US/10/335,977
APPLICATION NUMBER: US/10/335,977
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/993,002
FILING DATE: 17-DEC-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM IS09660
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: WINDOWS NT 4.0
SOFTWARE: UNIX
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                ORIGINAL SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                          FEATURE:
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210 KKRYEKEFNLLWVGLLGF
                                                                                                                         369 KKRYEKEFNILWVGLLGF 386
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                                                                                                                                                           1 KKRYDREF-----LLGF 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                      Score 44; DB Pred. No. 18;
                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                          4.
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GENERAL INFORMATION

APPLICANT: DOUGLAS SMITH et al

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NAME/KEY: misc feature;
LOCATION: (B) LOCATION 1...556;
SEQUENCE DESCRIPTION: SEQ ID NO: 6271:
US-10-335-977-6271
                                                                                                                                                                                                                                                                                                                                                                  US-10-437-963-114937
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                                                                                                                                                                                                                                                                                                      Sequence 114937, Application US/10437963 Publication No. US20040123343A1 GENERAL INFORMATION:
SEQ ID NO 114937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                 APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: L1, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
                                                                                                                                                                                                                                       APPLICANT: La Rosa, Thomas J. APPLICANT: Kovalic, David K. APPLICANT: Zhou, Yihua
                                                                                                                                                                                APPLICANT:
                     NUMBER OF SEQ ID NOS: 204966
                                                                                                                                                                                                                        APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 6271:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
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APPLICATION NUMBER: US/10/335,977
FILING DATE: 30-Dec-2002
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear MOLECULE TYPE: protein HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: GTN-018
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 08/993,002 FILING DATE: 17-DEC-1997 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORIGINAL SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  372 KKRYEKEFNLLWVGLLGF 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            l Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 KKRYDREF-----LLGF 12
                                                                                                                                                                                               Cao, Yor
Wu, Wei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC Compatible OPERATING SYSTEM: Windows NT 4.0
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STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (617)742-4214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 28 State Street
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                                                                                                                                                                                                                    Yongwei
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55.6%;
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Pred. No. 18;
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                                                                                                                     Associated With
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US-10-425-115-282367, Application US/10425115; Sequence 282367, Application US/10425115; Publication No. US20040214272A1; GENERAL INFORMATION:
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; FEATURE:
; OTHER INFORMATION: Clone US-10-437-963-114937
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                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Oryza sativa
US-10-259-194A-312
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                                                                                                                                                                                                  RESULT 11
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CURRENT APPLICATION NUMBER: US/10/259,194A
CURRENT FILING DATE: 2003-01-07
PRIOR APPLICATION NUMBER: US 60/325,277
PRIOR FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: US 60/370,743
PRIOR FILING DATE: 2002-04-04
PRIOR APPLICATION NUMBER: US 60/370,620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-259-194A-312
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          APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(53222)B
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CURRENT APPLICATION NUMBER: US/10/425,115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 662
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TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF PLANT GENES
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TYPE: PRT
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7; Conserv
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Briggs, Steven P.
Cooper, Bret
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ricke,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Provart, Nicholas
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Glazebrook,
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77.8%;
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Pred. No. 1.7e+02;
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Pred. No.
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57;
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                                                  Other Molecules Associated With
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US-10-334-143-69

; Sequence 69, Application US/10334143
; Publication No. US20040009549A1
; GENERAL INFORMATION:
; APPLICANT: GRIGORIEV, IGOR VYACHESLAVOVICH
; APPLICANT: SUDARSANAM, SUCHA
; TITLE OF INVENTION: METHOD FOR DETECTING REMOTE HOMOLOGUES AND
; TITLE OF INVENTION: KINASES IDENTIFIED WITH THE METHOD
; FILE REFERENCE: 038602/1543
; CURRENT APPLICATION NUMBER: US/10/334,143
; CURRENT FILING DATE: 2001-12-31
; PRIOR FILING DATE: 2001-12-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 282367
LENGTH: 950
TYPE: PRT
ORGANISM: Zea maye
FEATURE:
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US-10-437-963-187843
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Best Local Similarity 72...
Conservative
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SEQ ID NO 187843
LENGTH: 1516
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Best Local
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NAME/KEY: unsure
NAME/KEY: (1)..(1
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERENCE: 38-21(53221)B CURRENT APPLICATION NUMBER: US/10/437,963 CURRENT FILING DATE: 2003-05-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: La Rosa, Thomas J. APPLICANT: Kovalic, David K. APPLICANT: Zhou, Yihua
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OTHER INFORMATION: unsure at all Xaa locations
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                                                                                                                                                                                                                                                                                              552 RKRYSRDFLL 561
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Cao, Yongwei
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70.0%;
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Pred. No. 1.8e+02
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Pred. No. 2.8e+02;
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                                                                                                             AND NOVEL
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APPLICANT: TREMBLAY, MICHEL
APPLICANT: TREMBLAY, MICHEL
APPLICANT: TSUKIAYANA-KOKARA, KYOKO
FITTLE OF INVENTION: NON-HUMAN TRANSGENIC ANIMAL WHOSE GERM CELLS AND
FITTLE OF INVENTION: SOMATIC CELLS CONTAIN A KNOCKOUT MUTATION IN DNA
FILE REFERENCE: 514012000400
CURRENT APPLICATION NUMBER: US/09/973,473
CURRENT FILING DATE: 2001-10-03
PRIOR APPLICATION NUMBER: PCT/CA00/00388
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: 60/128,559
PRIOR APPLICATION NUMBER: 60/179,743
PRIOR APPLICATION NUMBER: 60/179,743
PRIOR FILING DATE: 2000-02-02
NUMBER OF SEQ ID NOS: 27
NUMBER OF SEQ ID NOS: 27
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FEATURE:
NAME/KEY: MOD RES
LOCATION: (2479)
OTHER INFORMATION: Variable amino acid
US-10-334-143-69
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US-09-973-473-12
; Sequence 12, Application US/09973473
; Publication No. US20030041341A1
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US-10-783-528-116
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Best Local Similarity
Matches 7; Conserv
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SOFTWARE: PatentIn Ver. 2
SEQ ID NO 69
                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: SONENBERG, Nahum
APPLICANT: TREMBLAY, Michel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn version 3.2 SEQ ID NO 116
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Best Local Similarity 63.6%;
Matches 7; Conservative
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APPLICANT: Gish, Kurt
APPLICANT: Wilson, Keith
APPLICANT: Zlotnik, Albert
TITLE OF INVENTION: METHODS OF DIAGNOSIS OF CANCER, COMPOSITIONS AND
FILE REFERENCE: 05882.0191.NEVS01
CURRENT APPLICATION NUMBER: US/10/783,528
CURRENT FILING DATE: 2004-02-19
NUMBER OF SEQ ID NOS: 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 2872
TYPE: PRT
ORGANISM: Homo Sapiens
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Pred. No. 5.5e+02;
2; Mismatches 2;
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Pred. No. 4.7e+02;
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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Perfect score:
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length: 2000000000
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Gapop 10.0 , Gapext 0.5
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ater than or equal to the score of the result being printed,
rived by analysis of the total score distribution.
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Match Length DB
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KKRYDREFLLGF 12
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US-09-270-767-40048
US-09-270-767-55264
US-09-270-767-55264
US-09-269-54333-7
US-09-248-796A-19839
US-09-248-796A-19839
US-09-248-796A-19839
US-09-270-767-58606
US-08-555-722-8
US-09-107-32A-6607
US-09-107-532A-6607
US-09-105-390-64
US-09-105-390-64
US-09-105-390-64
US-09-105-390-64
US-09-126-39351
US-09-248-796A-18814
US-09-252-93151
US-09-252-93151
US-09-256-2739
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US-09-949-016-8518

US-09-248-796A-27703

US-09-302-620B-106

US-09-911-781-24

US-10-400-902-24
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                                                                                                                                                                     Sequence 106, Appl
Sequence 24, Appl
Sequence 24, Appl
Patent No. 5204252
Patent No. 5204252
                 Sequence 40048, A
Sequence 5264, A
Sequence 14261, A
Sequence 1, Appli
Sequence 1839, A
Sequence 8459, Ap
Sequence 8459, Ap
Sequence 8606, A
Sequence 8, Appli
Sequence 8, Appli
Sequence 10766, A
Sequence 6607, Ap
Sequence 64, Appl
Sequence 4393, Ap
Sequence 4393, Ap
Sequence 23351, A
Sequence 23351, A
Sequence 23351, A
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Sequence 8518, Ap
Sequence 27703, A
Appli
Appli
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US-08-441-750-4	US-08-245-756-4	US-08-088-633-4	US-09-265-585C-50	US-09-186-188B-50	US-08-842-445-50	US-09-186-276B-50	US-09-265-585C-129	US-09-540-236-3246	US-09-265-585C-110	US-09-270-767-45396	US-09-270-767-43382	US-09-992-598-124	US-09-997-333-124	US-09-990-444-124	US-09-991-181-124	US-08-996-083-3	US-08-918-914-1
Sequence 4	Sequence 4	Sequence 4	Sequence 5	Sequence 5	Sequence 5	Sequence 5	Sequence 1	Sequence 3	Sequence 1								
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RESULT 1 US-09-264-512B-2

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PATENT NO. 6812359

PATENT NO. 6812359

GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASS
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF
FILE REFERENCE: CLOO1307

FULE REFERENCE: CLOO1307

CURRENT APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FRASESEQ for Windows Version 4.0

SEQ ID NO 8518

LENGTH: 977
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US-09-949-016-8518
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APPLICANT: Hentze, Matthias W.
APPLICANT: Hentze, Matthias W.
APPLICANT: Hentze, Ennio

APPLICANT: De Gregorio, Ennio

TITLE OF INVENTION: TRANSLATION DRIVER SYSTEM AND METHODS FOR USE THEREOF

FILE REFERENCE: 9892-004

CURRENT APPLICATION NUMBER: US/09/264,512B

CURRENT FILING DATE: 1999-03-08

CURRENT FILING DATE: 1999-03-08

NUMBER OF SEQ ID NOS: 13

SOFTWARE: PATENTIN Ver. 2.0

SEQ ID NO 2

LENGTH: 1560
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TYPE: PRT
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100.0%; Pred. No. 0.0015;
ative 0; Mismatches 0;
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3 OF DETECTIO
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APPLICANT: Tang, Maria
APPLICANT: Loper, John C.
APPLICANT: Gleeson, Martin
TITLE OF INVENTION: CYTOCHROME P450 MONOOXYGENASE AND NADPH CYTOCHROME P450
TITLE OF INVENTION: CYTOCHROME D450 MONOOXYGENASE RELATED TO THE OMEGA
TITLE OF INVENTION: HYDROXYLASE COMPLEX OF CANDIDA TROPICALIS AND METHODS
TITLE OF INVENTION: RELATING THERETO
FILE REFERENCE: 1010-16.seq
CURRENT APPLICATION NUMBER: US/09/302,620B
CURRENT FAPLICATION NUMBER: 1999-04-30
NUMBER OF SEQ ID NOS: 109
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 106
LENGTH: 267
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CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR FILING DATE: 1998-02-13
PRIOR FILING DATE: 1998-08-13
PRIOR PRIOR DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 27703
LENGTH: 82
TYPE: PRT
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US-09-302-620B-106
; Sequence 106, Application US/09302620B
; Patent No. 6331420
; GENERAL INFORMATION:
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; PEATURE;
; NAME/KEY: UNSURE
; LOCATION: (10)
; OTHER INFORMATION: Identity of amino acid sequences at the above locations are unkno US-09-248-796A-27703
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Best Local Similarity
Marches 10; Conserva
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US-09-248-796A-27703
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Best Local Similarity
Matches 8; Conserv
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                                                                                                                                                                                                                                                                                                        APPLICANT:
                                                                                                                                                                                                                                                                                                                                         APPLICANT: Wilson, C. Ron
APPLICANT: Craft, David L.
APPLICANT: Eirich, Dudley
APPLICANT: Eshoo, Mark
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                        APPLICANT:
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                                                                                                                                                                                                                                                                                     Madduri, Krishna M. Cornett, Cathy A. Brenner, Alfred A.
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66.7%;
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Pred. No. 0.12;
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NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 24
; LENGTH: 267
; TYPE: PRT
; ORGANISM: Candida tropicalis
US-10-400-902-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Craft, David L.
APPLICANT: Wilson, C. Ron
APPLICANT: Eirich, Dudley
APPLICANT: Eirich, Dudley
APPLICANT: Zhang, Yeyan
TITLE OF INVENTION: USE OF CYP52A2A PROMOTER TO
FILE REFERENCE: U0012 OS/OAAP (1010-49)
CURRENT APPLICATION NUMBER: US/09/911,781
CURRENT FILING DATE: 2001-07-24
NUMBER OF SEQ ID NOS: 34
SOFTWARE: Patentin version 3.1
SEQ ID NO 24
LENGTH: 267
TYPE: PRT
                                                                                                                                                                                                  Sequence 24, Application US/10400902

Patent No. 6790640

GENERAL INFORMATION:
APPLICANT: Wilson, C. Ron
APPLICANT: Wilson, C. Ron
APPLICANT: Eirich, Dudley
APPLICANT: Zhang, Yeyan

TITLE OF INVENTION: USE OF CYP52A2A PROMOTER TO
FILE REFERENCE: U0012 OS/OAAP (1010-49)
CURRENT FILING DATE: 203-03-31
PRIOR APPLICATION NUMBER: US/10/400,902
CURRENT FILING DATE: 203-03-31
PRIOR APPLICATION NUMBER: US/09/911,781
PRIOR FILING DATE: 2001-07-24
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Best Local Similarity
Watches 6; Conserve
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GENERAL INFORMATION:
                                    Matches
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                                Local Similarity
hes 6; Conserv
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75.0%;
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                                                 Score 37; DB Pred. No. 34;
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175 DREFVIGE 182

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RESULT 8
5204252-4
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;PATENT NO. 5204252
;PATENT: CREGG, JAMES M.;GLEESON, MARTIN A.;HAAS, LISA
;PICATAGGIO, STEPHEN
TITLE OF INVENTION: CANDIDA TROPICALIS TRANSFORMATION SYSTEM
; NUMBER OF SEQUENCES: 9
; CURRENT APPLICATION DATA:
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PARPLICANT: CREGG, JAMES M.; GLEESON, MARTIN A.; HAAS, LISA
PICATAGGIO, STEPHEN

TITLE OF INVENTION: CANDIDA TROPICALIS TRANSFORMATION SYSTEM
NUMBER OF SEQUENCES: 9
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/386,837
FILING DATE: 27-JUL-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 308,481
; FILING DATE: 08-FEB-1989
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                                                                          Sequence 40048, Application US/09270767

Patent No. 6703491

GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 40048
LENGTH: 347
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Best Local Similarity
Matches 6; Conserv
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Best Local Similarity
Matches 6; Conserv
-09-270-767-40048
                                             TYPE: PRT ORGANISM: Drosophila melanogaster
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APPLICATION NUMBER: 308,481
FILING DATE: 08-FEB-1989
              OTHER INFORMATION: Xaa means any amino acid
                                FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/07/386,837 FILING DATE: 27-JUL-1989
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Conservative 2
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Pred. No.
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US-09-902-540-14261
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US-09-270-767-55264
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                                                                                                                        ; ORGANISM: Myxococcus xanthus US-09-902-540-14261
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Best Local S
Matches 7
                                                                                                                                                                APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
FILE REFERENCE: 38-10(15849)B
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 14261
LENGTH: 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 55264
LENGTH: 347
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                        Sequence 14261, Application US/09902540 Patent No. 6833447 GENERAL INFORMATION:
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                                                          Query Match
Best Local Similarity
Matches 7; Conserv
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Xaa means any amino acid
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                                                                                                                                                        TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                66 RYDRSILLG 74
 120 KSFDREFLL 128
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                              2 KRYDREFLL 10
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Hinkle, Gregory J.
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Pred. No.
                                                                            Score 37; Pred. No.
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Pred. No. 46;
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RESULT 12 US-08-954-333-7

; Sequence 7, Application US/08954333

Patent No. 5986080

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; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (602)
; OTHER INFORMATION: Identity of amino acid sequences at the above locations are
US-09-248-796A-19839
                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-248-796A-19839
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GENERAL INFORMATION:
                                                                                                                       SEQ ID NO 19839
LENGTH: 602
TYPE: PRT
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Best Local
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                                                                                                                                                                           FILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR FILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR FILING DATE: 1998-08-13
NUMBER: OF SEQ ID NOS: 28208
                                                                                                                                                                                                                                                                                                                                       APPLICANT: Keith Weinstock et al TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (414) 271-355
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 599 amino acids
TYPE: amino acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                  ORGANISM: Candida albicans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Ryser, David G.
REGISTRATION NUMBER: 36,407
REFERENCE/DOCKET NUMBER: 65:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (414) 277-5717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Milwaukee
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(414) 271-3552
77 TN NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             411 East Wisconsin Avenue
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VENTION: CLONED NUCLEOTIDE PYROPHOSPHOHYDRALASE AND
VENTION: USES THEREOF
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FILE REFERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 8459
LENGTH: 451
TYPE: PRT
ORGANISM: Klebsiella pneumoniae
US-09-489-039A-8459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Thes 6; Conserve
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Search completed: November 29, 2005, 23:04:21 Job time : 30.6364 secs
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                                                                                                                                                                                     ; ORGANISM: Drosophila melanogaster US-09-270-767-58606
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US-09-270-767-58606
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                                                                                                                                                                                                                              APPLICANT: Homburger et al.

TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 58666
LENGTH: 55
                                                                                                                                                                                                                                                                                                                                                                      Sequence 58606, Application US/09270767 Patent No. 6703491 GENERAL INFORMATION:
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APPLICANT: Gary Bro
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Patent No. 661083
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TITLE OF INVENTION: NUCLECIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2004001
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Copyright (c) 1993 - 2005 Compugen Ltd

November 29, 2005,

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Mammalia; Butheria; Buarchontoglires; Glires; Lagomorpha; Leporidae;

Oryctolagus.

NCBI_TaxID=9986;

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                                                                                                                                                               Sus scrofa (Pig).
Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suida
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PubMed=15448358; DOI=10.1099/vir.0.80254-0;
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Scoring

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Result

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Description

SUMMARIES

Q6EVH7 RABIT
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Q6EVI2 HOVIN
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Q6EVH9 MOUSE
IF4G1 RABIT
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Strong R., Belsham G.J.;
"Sequential modification of translation initiation factor
NUCLEOTIDE SEQUENCE.
PubMed=15448358; DOI=10.1099/vir.0.80254-0;
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L; AJ746223; CAG34103.1; -; mRNA.
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Eukaryota; Metazoa; Chordata; Crania
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Strong R., Belsham G.J.;
"Sequential modification of translation ini
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25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
EIF4GI protein (Fragment).
Name=Elf4gl; Synonyms=eIF4GI;
Nus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Strong R., Belsham G.J.;
"Sequential modification of translation initiation factor eIF4GI
"Sequential modification of translation initiation factor eIF4GI
two different foot-and-mouth disease virus proteases within infec
BHK cells; identification of the 3Cpro cleavage site.";
J. Gen. Virol. 85:2953-2962 (2004).
EMBL; AJ746222; CAG34102.1; -; mRNA.
MGI; MGI:2384784; Eif4g1.
                                                                                                                                                                                             01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Eukaryotic translation initiation factor 4 ga
(eIF-4G1) (eIF-4G 1) (p220).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurogna
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                                                                                                                                  Name=EIF4G1; Synonyms=EIF4G;
Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE.
PubMed=15448358; DOI=10.1099/vir.0.80254-0;
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                                                                                                                                                                                                                                                                                                           ĪF4G1 RABIT
P41110;
    NUCLEOTIDE
STRAIN=New
                                                         Oryctolague.
NCBI_TaxID=9986;
                                                                                                           Mammalia; Eutheria;
                                                                                                                             Eukaryota, Metazoa;
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175 AA;
    SEQUENCE, AND Zealand white;
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19532 MW; BC221DC60B116A6E CRC64;
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AND PROTEIN SEQUENCE
hite; TISSUE-Brain;
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Pred. No. 0.0
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Pred. No. 0.00061;
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RESULT 9
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DT 01-MAR-2004 (T
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Pfam; PF02854; MIF4G; 1.
Pfam; PF020200; W2; 1.
SMART; SM00515; eIF5C; 1.
SMART; SM00544; MA3; 1.
SMART; SM00543; MIF4G; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                involved in the recognition of the mRNA cap, ATP-dependent unwinding of 5'-terminal secondary structure and recruitment of mRNA to the ribosome.

SUBUNIT: eIF4F is a multi-subunit complex, the composition of which varies with external and internal environmental conditions. It is composed of at least EIF4A, EIF4B and EIF4Al or EIFA2, Interacts with eIF3, mutually exclusive with EIF4Al or EIFA2, EIF4E and through its N-terminus with PAPBG1. Interacts through its N-terminus with PAPBG1. Interacts through its N-terminus with PAPBG1. Interacts through its SC-terminus with the serine/threonine kinases MKNK1, and with MKNK2. Appears to act as a scaffold protein, holding these enzymes in place to phosphorylate EIF4E (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lamphear B.J., Yan R., Yang P., Waters D., Liebig H.-D., Kl Kuechler E., Skern T., Rhoads R.E.;
"Mapping the cleavage site in protein synthesis initiation 4 gamma of the 2A proteases from human Coxsackievirus and Thinovirus.";
                                                                                                                                                                                                                                                             MOD_RES
MOD_RES
SEQUENCE
                                                                                                                                                                                                                                                                                                    Direct protein sequencing; Initiation factor; I Protein biosynthesis; RNA-binding; Translation COMPBIAS 188 192 POLY-Glu.
COMPBIAS 262 275 Poly-Glu.
COMPBIAS 1393 1398 Poly-Glu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This Swiss-Prot entry is copyright. It is produced through a converge the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             eIF-4 gamma.";
J. Biol. Chem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro;
InterPro;
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SMR; P41110; 1036-1367
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MEDLINE=93054654; PubMed=1429670;
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long as its content is in no way
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12; Conserv
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IPR003890; IF_eIF4G.
IPR003891; IF_eIF4G_MA3
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ation factor 4GI (Frac
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Pfam; PF02847; MA3; 1
Pfam; PF02854; MIF4G;
Pfam; PF02020; W2; 1.
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SMR; Q7YS39; 574-814.

GO; GO:0003723; F:RNA binding; IEA.

GO; GO:0003743; F:translation initiation facto

GO; GO:0003743; P:protein biosynthesis; IEA.

GO; GO:0006412; P:regulation of translational

InterPro; IPR003307; eIF5C.
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HSSP;
SMR; GG
GO; GG
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GO; GG
                                           "Human eukaryotic translation initiation two separate and independent binding site Mol. Cell. Biol. 17:6940-6947(1997).
                                                                                                      MEDLINE=98038763; PubMed=9372926; Imataka H., Sonenberg N.;
                                                                                                                                                                         NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM E), INTERACTION WITH EIF4A, MUTAGENESIS OF LEU-769; LEU-772; PHE-777; 843-LEU-LEU-844; 852-PHE-GLU-852; LEU-897; ILE-903; LEU-906; ARG-975; PHE-978; LI
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Mammalia; Eutheria;
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Eukaryota, Metazoa, Chordata,
    NUCLEOTIDE
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SM00544;
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IPR003891; IF_eIF4G_MA3.
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1423 AA;
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[MRNA] (ISOFORM B),
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RA Wakamatsu A., Hayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S., Ra Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S., Ra Yamamoto J.-I., Saito K., Kawai Y., Isono Y., Nakamura Y., Ra Yamamoto J.-I., Saito K., Yasuda T., Isono Y., Nakamura Y., Ra Shiratori A., Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Ra Shiratori A., Sudo H., Kanda K., Yokoi T., Furuya T., Kikawa E., Omura Y., Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Pujimori K., Tanai H., Kimata M., Watanabe M., Hiraoka S., Chiba Y., Ishibashi T., Yamashita H., Murakawa K., Ra Fujimori K., Tanai H., Kimata M., Watanabe M., Hiraoka S., Chiba Y., Tanikawa M., Komai S., Komai F., Hara R., Takeuchi K., Arita M., Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K., Arita M., Ra Timose N., Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S., Amori Y., Mosashino K., Yuuki H., Goto Y., Shimizu F., Wakebe H., Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B., Yamazaki M., Watanabe T., Sugiyama A., Takemoto M., Kawakami B., Pujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T., Yamazaki M., Watanabe T., Sugiyama A., Takemoto M., Kawakami B., Pujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T., Yamazaki M., Matanabe T., Kobatake N., Inagaki H., Ikema Y., Okamoto S., Ra, Akawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S., Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T., Ra, Akawabata A., Hata H., Watanabe M., Komatsu T., Nakagawa K., Ra, Nukajima Y., Matanabe M., Tashiro T., Morinaga M., Sasaki M., Ra, Makai K., Yada T., Nakamura Y., Ohara O., Isogai T., Nakagawa K., Ra, Nakai M., Watanabe T., Shirai Y., Takahashi Y., Nakagawa K., Ra, Nakai M., Watanata Y., Ohara O., Isogai T., Sugano S., Takana T., Nakamura Y., Ohara O., Isogai T., Sugano S., Takana T., Nakagawa M., Tashita M., Masuho Y., Yamashita R., Nakai M., Tashita M., Masuho Y., Yamashita R., Nakai M., Tashita M., Masuho Y., Yamashita R., Nakai M., Tashita M., Masuho Y., Yamashita R., 
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                                                                                                                                                                                                                                                                                                                                                                                            The German cDNA consortium; Submitted (JAN-2005) to the
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Byrd M.P., Zamora M., Lloyd R.E.;
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AND 617-LEU-LEU-618.
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                                                                                                                     Biol.
                                                                                                                    mammalian cells.";
Biol. 21:743-754(2001).
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translation by 4E-binding protein
nding to eukaryotic initiation fac
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                                                                                X MEDLINE-57BL/6; TISSUE-Brain, and Fetal brain;

XX MEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

XX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

XX Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

XX Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

XX Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

XX Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

XX Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

XX Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

XX Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

XX Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hong L.,

XX Altschul S.F., Jordan B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

XX Altschul S.F., Jordan B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

XX Altschul S.F., Jordan B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

XX Altschul S., Morley R.C., Heterson K.J., Malek J.A., Gunaratne P.H.,

XX Altschul S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

XX Altschul S., Worley K.C., Hale S., Garcia A.M., Gybbs R.A.,

XX Altschul S., Worley R.C., Hale S., Garcia A.M., Gybbs R.A.,

XX Altschul S., Worley R.C., Shevchenko Y., Bouffard G.G.,

XX Altschul S., Worley R.W., Touchman J.W., Green E.J., Lu X., Gibbs R.A.,

XX Altschul S., Worley R.W., Touchman J.W., Green B.D., Dickson M.C.,

XX Altschul S., Krzywinski M.I., Skalska U., Smailus D.E.,

XX Babey J., Helton S., Krzywinski M.I., Skalska U., Smailus D.E.,

XX Babey J., Schmutz J., Myers R.M.,

**Generation and initial analysis of more than 15,000 full-length human

XX McDiller C.D., State R.M., Schen S., Sanchez A.,

XX P., Schmutz J., Marra M.A.,

**Touchman J.W., Schmutz J., Myers R.M.,

**Touchman J.W., Schmutz J., Myers R.M.,

**Generation and initial analysis of more than 15,000 full-length human

XX McDiller C.,

XX Altschul S., Schmutz J., Myers R.M.,

XX Altschul S., Schmutz J., Myers R.M.,

XX Altschul S., Schmutz J., Mye
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X-RAY CRYSTALLOGRAPHY (2.38 ANGSTROMS)
ROTAVIRAL NSP3, INTERACTION WITH PABP,
ILE-182; ILE-192 AND ILE-196.
ILE-182; ILE-197 AND ILE-197 AND ILE-197 AND ILE-198 AND ILE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          X-RAY CRYSTALLOGRAPHY (2.24 ANGSTROMS) OF 13 Bellsolell L., Cho-Park P.F., Poulin F., Sor "Two HEAT domains in the C-terminal portion binding to EIF4A and MNKI.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Groft C.M., Burley S.R. "Recognition of eIF4G circularization.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ĪF4G1 MOUSE STANDARD; PRT; 1600 AA. Q6NZJĒ; Q6NZNB; Q8BW99; 13-SEP-2005 (Rel. 48, Last sequence update) 13-SEP-2005 (Rel. 48, Last annotation update) 13-SEP-2005 (Rel. 48, Last annotation date) Eukaryotic translation initiation factor 4 gar
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PubMed=12086624; DOI=10.1016/S1097-2765(02)00555.
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Mammalia; Eutheria; Euarchontoglires; Glires;
Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10090;
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FUNCTION: Component of the protein complex eIF4F, which is involved in the recognition of the mRNA cap, ATP-dependent unwinding of 5',-terminal secondary structure and recruitment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mRNA to the ribosome.
SUBUNIT: eIF4F is a multi-subunit which varies with external and int
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Sonenberg N., Burley
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A Birney E., Hayashizaki Y.;

RT 60,770 full-length cDNAs.";

RI 60,770 full-length cDNAs.";

RL Nature 420.563-573(2002).

CC -i- FUNCTION: Component of the protein complex eIF4F, which is involved in the recognition of the mRNA cap, ATP-dependent of unwinding of 5'-terminal secondary structure and recruitment of mRNA to the ribosome (By similarity).

CC -i- SUBUNIT: eIF4F is a multi-subunit complex, the composition of the subunit complex, the composition of the subunit complex and EIF4G1/EIF4G3.

CC It is composed of at least EIF4A, EIF4E and EIF4G1/EIF4G3.

CC It is composed of at least EIF4A, EIF4E and EIF4G1/EIF4G3.

CC EIF4E and through its N-terminus with PAPBC1. Interacts through the CC its C-terminus with the serine/threonine kinases MRNK1, and with place to phosphorylate EIF4E. Non-phosphorylated EIF4EBP1 competes with EIF4G1/EIF4G3 to interact with EIF4G1/EIF4G3 to interact with EIF4G1/EIF4G3 to interact strate insulin stimulated MAP-kinase (MAPK1 and MAPK3) phosphorylation of EIF4G1/EIF4G3 to bind and consequent initiation of translation (By similarity).
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RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Baldarelli R., Hill D.P., Bult C., Chothia C., Corbani L.E., Cousins S.,
RA Baldarelli R., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Gasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Magdohima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Mayashima T., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA Wilning L.G., Wynshaw-Boris A., Yanagisawa M., Yangi J., Yangi Sawa M., Sakazume N., Sato K.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Hiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Minaya E., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miraky E., Hayashizume W., Jasaki D., Shibata K., Shinagawa A.,
RA Miraya E., Laki Y., Sasaki D., Shibata K., Shinagawa A.,
RA Miraya E., Hashizume W., Waterston R., Lander E.S., Rogers J.,
RA Miraya E., Hashizume W., Waterston R., Lander E.S., Rogers J.,
                                                                                                                                                                                                                                                                                                                                                                                                    EMBL;
MGI; MGI:2384784; Eif4g1.

GO; GO:0005737; C:cytoplasm; IDA.

InterPro; IPR003397; eIF5C.

InterPro; IPR003890; IF eIF4G.

InterPro; IPR003891; IF eIF4G MA3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY: Belongs to the eIF\overline{4}G fam SIMILARITY: Contains 1 MIF4G domain.
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                                                                                                                                                                                                                                            ; BC066038; AAH66038.1; -; mRNA.; BC066103; AAH66103.1; -; mRNA.; BC079675; AAH79675.1; -; mRNA.; RX053144; BAC35282.1; -; mRNA. Q6NZJ6; 755-995; 1234-1565. Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Event=Alternative splicing; Named isoforms=2;
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RESULT 13
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QARYZ6_TETNG PRELIMINARY;
AC QARYZ6;
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DT 13-SEP-2005 (TrEMBLrel. 31,
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Best Local
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SMART; SM00544; MA3; 1.
SMART; SM00543; MIF4G; 1.
Alternative splicing; Initiation factor; Phosphorylation;
Alternative splicing; RNA-binding; Translation regulation
Protein biosynthesis; RNA-binding; Translation regulation
MIF4G.

DARPCI-binding (By similarit
DARPCI-binding (By similarit
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13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
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13-SEP-2005 (TrEMBLrel. 31, Last annotation updat
EIF4G1 variant protein (Fragment).
Name=EIF4G1 variant protein;
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
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Q4LE58;
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Pfam; PF02020; W2; 1.
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Phosphoserine (By similarity).
Missing (in isoform 2).
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Pred. No. 0.0062;
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Missing (in isoform 2).
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Necessary but not sufficient for MKNK1-
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W; 8664A8B449C7A128 CRC64;
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Asp/Glu-rich.
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Best Local S
Matches 11
   Bird C.;
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EMBL; AL666477; CAI12535.1; -
EMBL; AL358392; CAI12158.1; -
EMBL; AL358392; CAI12535.1; J
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Chromosome 16 (Fragment).
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NUCLEOTIDE SEQUENCE.

Genoscope; Whitehead Institute Centre for Genome Research;
Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.

-I- CAUTION: The sequence shown here is derived from an
-I- CAUTION: The sequence shown here is derived from whitehead the sequence should be should be sequence.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetradontoidea; Tetraodontidae; Tetraodon.
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QSSWD1;
Q1-FEB-2005 (TrEMBLrel. 29, Created)
Q1-FEB-2005 (TrEMBLrel. 29, Last sequence update)
Q1-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Eukaryotic translation initiation factor 4 gamma, 3
NamesEIF4G3; QRYMAMESSRP11-190H11.1-007;
Homo sapiens (Human)
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CO Eukaryot
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OC Mammalia
OC Cercopit
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13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
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13-SEP-2005 (TrEMBLrel. 
                                                                                                                                                                                                                                                                                                                                                                                 Osada N., Hirata M., Tanuma R., Kusuda J., Hida M., Suzuki Y., Sugano S., Gojobori T., Shen J.C.-K., Wu C.I., Hashimoto K.; Subano S. and structural divergence of 5'UTR evolution: Comparative analysis between human and cynomolgus monkey cDNAs."; Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases. EMBL, AB179159; BAE02210.1; -; mRNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              International consortium for macaque cDNA "DNA sequences of macaque genes expressed evolutionary implications.";
Submitted (JUN-2005) to the EMBL/GenBank/I
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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64
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1: pir1:*
2: pir2:*
3: pir3:*
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KKRYDREFLLGF 12
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Copyright (c) 1993 - 2005 Compugen Ltd
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G72629
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G7363400
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T48510
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C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 14-Feb-1997 #sequence_revision 14-Feb-1997 #text
C;Accession: 146707
R;Yan, R; He, W; Rhoads, R.E.
J. Biol. Chem. 268, 19200-19203, 1993
A;Title: Mapping the cleavage site in protein synthesis A;Reference number: 146707; MUID:93374895; PMID:8336129
A;Accession: 146707

146707

translation initiation factor eIF4-gamma - rabbit

#text_change 09-Jul-2004

initiation

factor eIF-4 gamma

Q.

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C;Species: Homo sapiens (man)
C;Date: 10-Unn-1993 #sequence_revision 18-Nov-1994 #text_change 08-Dec-1994
C;Accession: A44453
R;Yan, R.; Rychlik, W.; Etchison, D.; Rhoads, R.E.
J. Biol. Chem. 267, 23226-23231, 1992
A;Title: Amino acid sequence the human protein synthesis initiation factor eIF-4 gamman A;Reference number: A44453; MUID:93054654; PMID:1429670
A;Accession: A44453
                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT
A44453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1402 <VAN>
                                                                                                                                                  A;Molecule type: nucleic acid
A;Residues: 1-1396 <7AN>
A;Residues: 1-1396 <7AN>
A;Cross-references: UNIPARC:UPI000017C3F3
A;Note: sequence inconsistent with the nucleotide translation
A;Note: sequence extracted from NCBI backbone (NCBIP:118286)
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Similarity 80.0%;
12; Conservative
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Pred. No. 0.00071;
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C;Species: Helicobacter pyron-
A;Variety: strain J99
A;Variety: strain J99
C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
C;Accession: G71892
C;Accession: G71892
R;Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, R;Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Jiang, Q.; Taylor, D.E.; Vovis, Tres. C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, Tres. C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, Tres. C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, Tres. C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, Tres. C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, Tres. C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, Tres. C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, Tres. C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, Tres. C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, Tres. C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, Tres. C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, Tres. C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, Tres. C.; Gibson, R.; Mills, S.D.; Jiang, R.; Mills, R.; Mi
                                                                                           hypothetical protein PH0309 - Pyrococcus horikoshii C;Species: Pyrococcus horikoshii C;Species: Pyrococcus horikoshii C;Species: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 09-Jul-2004 C;Accession: G71456
R;Kawarabayasi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamol M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida DNA Res. 5, 55-76, 1998
A;Title: Complete sequence and gene organization of the genome of a hyper-tl A;Reference number: A71000; MUID:98344137; PMID:9679194
A;Accession: G71456
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R;Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D. Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenne son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L. Nature 388, 539-547, 1997

A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C. A;Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.

A;Reference number: A64520; MUID:97394467; PMID:9252185

A;Accession: B64622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: DNA
A;Residues: 1-553 <ARN>
A;Cross-references: UNIPROT:Q9ZL24;
A;Experimental source: strain J99
C;Genetics:
A;Gene: jhp0757
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Nature 397, 176-180, 1999
A;Title: Genomic sequence comparison of two unrelated isolates
A;Reference number: A71800; MUID:99120557; PMID:9923682
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   A;Residues:
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                                                              A; Status: preliminary; nucleic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Residues: 1-553 <T
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                                                                                                                                                                                                                                             Y.; Yamamoto, J.; Kushida,
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translation initiation factor eIF-4 gamma homolog F27H5.30 [similarity] - A ;Alternate names: protein F27H5.30 [similarity] - A C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 09-Jul-2004 C;Accession: T49219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Accession: 153032
R;Chen, D.; Feng, J.O.; Feng, M.; Harris, M.A.; Mahy, P.; Mundy, DNA Cell Biol. 14, 235-239, 1995
A;Title: Sequence and expression of bone morphogenetic protein 3
A;Reference number: I53032; MUID:95186061; PMID:7880444
A;Accession: 153032
                                                                                                                                                                                   A;Residues: 1-1606 <RIE>
A;Cross-references: UNIPROT:Q9LY39; UNIPARC:UPI000009C67C;
A;Experimental source: cultivar Columbia; BAC clone F27H5
                                                                                                                                                                                                                                                                              R;Rieger, M.; Mueller-Auer, S.;
submitted to the Protein Sequenc
A;Reference number: Z25018
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T49219
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A;Residues: 1-360 <RES>
A;Cross-references: UNIPARC:UPI0000170CBA; GB:S77492; NID:g957225;
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I53032
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A;Note: this accession replaces an C;Genetics:
A;Gene: PH0309
                                                                                                                   A;Map position: 3
A;Introns: 455/3; 1370/2; 1435/2; 1523/1; 1529/1; 1558/3; 1586/2
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C;Superfamily: inhil
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e, April 2000
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DNA-directed DNA polymerase (EC 2.7.7.7) zeta chain - C;Species: Mus musculus (house mouse)
C;Date: 15-Oct-1999 #sequence raviator 15 Oct 100 "...
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R;Van Sloun, P.P.H.; Romeijn, R.J.; Eeken, J.C.J
Mutat. Res. 433, 109-116, 1999
                                                                                                  C;Accession: T09072
R;Hernandez, G.; Castellano, M.M.; Agudo, M.; Sierra, J.M. Eur. J. Biochem. 253, 27-35, 1998
A;Title: Isolation and characterization of the cDNA and the A;Reference number: Z16553; MUID:98237569; PMID:9578457
A;Accession: T09072
                                                                                                                                                                                                                              probable translation initiation factor eIF-4 gamma - fruit fly (Drosophila melanogaster) N;Alternate names: translation initiation factor eIF4G C;Species: Drosophila melanogaster C;Species: Drosophila melanogaster C;Date: 11-Jun-1999 #text_change 09-Jul-2004 C;Date: In-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
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A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A;Reference number: A33650; MUID:20512582; PMID:11058132
A;Accession: G83933
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A;Cross-references: UNIPROT:Q61493, UNIPARC:UPI0000028721; EMBL:AF083464; NID:g4079830;
A;Experimental source: strain 129/Ola; testis
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                A;Residues: 1-1666 <HER>
A;Cross-references: UNIPROT:O61380; UNIPARC:UPI000007DECF; EMBL:AF030155; NID:g3056722;
                                                             A; Molecule type: mRNA
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;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
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2; Mismatches
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A;Residues: 1-1418 <POH>
A;Residues: 1-1418 <POH>
A;Residues: 1-1418 <POH>
A;Residues: 1-1418 <POH>
A;Cross-references: UNIPROT;Q12267; UNIPARC:UPI000005327B; EMBL:Z73258; NID:g1360454; pff
A;Experimental source: strain S288C
A;Experimental source: strain S288C
A;Benes, V.; Rechmann, S.; Nentwich, U.; Schwager, C.; Ansorge, W.; Voss, H.
submitted to the protein Sequence Database, May 1996
A;Reference number: S64920
A;Accession: S64920
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S64918
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A;Map position: 4
C;Keywords: protein biosynthesis
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C; Superfamily: c
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A; Residues: 1-332 < RES>
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J. Gen. Microbiol. 139, 1753-1759, 1993
A;Title: The DNA sequence and minimal replicon of the Corynebacterium glutamicum plasmid
A;Reference number: I40726; MUID:94014972; PMID:8409918
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    Score 37.5;
Pred. No. 1.
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C;Date: 18-Aug-1995 #sequence__collection. C;Accession: D64133
C;A
prolyl-tRNA synthetase NMB1339 [imported] - Neisseria meningitidis (strain MC58 serogrou
C;Species: Neisseria meningitidis
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C;Accession: C81094
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C;Superf
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A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropy: A;Reference number: A72450; MUID:99310339; PMID:10382966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: UNIPROT:Q9YBV5; UNIPARC:UPI000005DF8A; DDBJ:AP000061; NID:g5104821; A;Experimental source: strain K1
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C;Species: Aeropyrum pernix
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 05-Oct-2004
C;Accession: G72629
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A; Residues: 1-212 <TIGR>
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H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; F
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R;Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.Å. Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.; ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M. science 287, 1809-1815, 2000

Science 287, 1809-1815, 2000

A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Vet A;Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.

A;Reference number: A81000; MUID:20175755; PMID:10710307
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                                                                                                                                                                  A;Gene: NMB1339
C;Superfamily: I
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A;Cross-references: UNIPROT:Q9JZ14; UNIPARC:UPI00000C46B1;
A;Experimental source: serogroup B, strain MC58
C;Genetics:
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A;Status: preliminary
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Search completed: November 29, 2005, 23:02:30 Job time: 20.8182 secs

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re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.
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1: geneseqp1980
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Copyright (c) 1993 - 2005 Compugen Ltd
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geneseqp2004s:*
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geneseqp2002s: *
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46.030 Million cell updates/sec
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Aab31450 Peptide d
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38	39	39	39	39	39	39	39	40	40	40	40	40	40	40	40	42	44	44	45	48
59.4	60.9	60.9	60.9	60.9	60.9	60.9	60.9	62.5	62.5	62.5	62.5	62.5	62.5	62.5	62.5	65.6	68.8	68.8	70.3	75.0
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AAY59752	ABB72054	ADB10592	ADB10594	ADB10596	ADS28271	AAB84406	AAB11101	ADE09353	ADE09433	ADX07307	ADR46703	ADR15681	ADK40962	ADC54131	ADI45381	ABM86083	AAW20906	AAW20422	AAB31451	ADQ97959
Aay59752 Human nor				Ţ		-		-	Novel	Суст				Eukary	•	Kice	, H	: :	jeż	-

RESULT 1 AAB31445 AAB31445 standard; peptide; 12 AA. 20-APR-2001 AAB31445; (first entry)

Binding peptide; cell death; cell Peptide derived from human eukaryotic Initiation Factor 4G (eIF4G). eukaryotic Initiation Factor 4G; eIF4G; eIF4E; apoptosis; anticancer; antitumor.

Homo sapiens.

WO200078803-A2.

28-DEC-2000.

21-JUN-2000; 2000WO-GB002414.

21-JUN-1999; 99GB-00014480

(UYDU-) UNIV DUNDEE.

Proud CG, Herbert TP, Lane DΡ, Fahraeus

WPI; 2001-071386/08.

Use of eukaryotic Initiation Factor 4E (elF4E) binding agents e.g. elF4E-binding peptide (elF4E-BP) derivatives as anticancer or antitumor agents for inducing apoptosis in e.g. mammalian tumor cells.

Example; Fig 5; 46pp; English.

The present sequence represents a peptide derived from an eukaryotic Initiation Factor 4G (eIF4G) protein. The specification describes elf and eIF4E binding agents, such as peptides or peptidemimetics. These binding agents are used for the induction of cell death. The binding peptides are used for inducing cell apoptosis. They are used in pharmaceutical compositions for anticancer or antitumor treatment of mammalian cells. Specifically, the peptides result in growth inhibitiof, or increased cytotoxicity to tumour cells inhibition eIF4G

Sequence 12 AA;

Query Match

100.0%; Score 64; 밁 4 Length 12;

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RESULT 2
AAB31438
ID AAB3
XX AAB3
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XX Bind
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Matches 1
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                                                                                                                                                                                                                                                                                                                                                                 Sequence 12
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                                                                                             AAB31450;
                                                                                                                              AAB31450 standard; peptide; 14 AA
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                        Peptide derived from human
                                                         20-APR-2001
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                        eukaryotic
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anticancer; antitumor.
                                                                                                                                                                                                                                                                                       Score 64; DB 4; -
Pred. No. 9.7e-05;
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hes 0;
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                    Factor
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                                                                                                                                               19-OCT-2000
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The present sequence represents a peptide derived from an eukaryotic Initiation Factor 4G (eIF4G) protein. The specification describes elf and eIF4E binding agents, such as peptides or peptidemimetics. These binding agents are used for the induction of cell death. The binding peptides are used for inducing cell apoptosis. They are used in pharmaceutical compositions for anticancer or antitumor treatment of mammalian cells. Specifically, the peptides result in growth inhibitiof, or increased cytotoxicity to tumour cells. note: the peptide is biotinylated and linked to penetratin
                                                                                                                                                                                                                                                                                                                Eukaryotic initiation factor; eIF4E; transgenic animal; antidiabetic; knockout mutation; 4E-BP1; glucose metabolism; fat metabolism; anorec drug; anti-obesity; anti-fat deposition; anti-metabolic.
09-APR-1999; 99US-0128559P. 02-FEB-2000; 2000US-0179743P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Use of eukaryotic Initiation Factor 4E (elF4E) binding agents e.g. elF4E-binding peptide (elF4E-BP) derivatives as anticancer or antitumor agents for inducing apoptosis in e.g. mammalian tumor cells.
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                                                                                   07-APR-2000; 2000WO-CA000388.
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Pred. No.
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RESULT 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
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16-FEB-2001
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Non-human transgenic animal useful as model for studying lipid and glucose metabolism, has germ and somatic cells containing knockout mutation in DNA encoding eukaryotic initiation factor 4E-binding pr
                                                                                                                                                                                                                                                                                                                                               Eukaryotic initiation factor; eIF4E; transgenic animal; antidiabetic; knockout mutation; 4E-BP1; glucose metabolism; fat metabolism; anorec drug; anti-obesity; anti-fat deposition; anti-metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB11100 standard;
                                                                                                                                                                 09-APR-1999; 99US-0128559P
02-FEB-2000; 2000US-0179743P
                                                                                                                                                                                                                 07-APR-2000; 2000WO-CA000388
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                                                                                                                                                                                                                                                                                                                Danio rerio
                                                                     WPI; 2000-672657/65
                                                                                             Sonenberg N,
                                                                                                                                                                                                                                                                                                                                                                                                              Zebrafish eIF-4E recognition motif peptide zeIF4G.
                                                                                                                                   (UYMC-) UNIV
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(first entry)
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Pred. No. 0.00013;
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryotic initiation factor; eIF4B; transgenic animal; antidiabetic; knockout mutation; 4B-BP1; glucose metabolism; fat metabolism; anorec drug; anti-obesity; anti-fat deposition; anti-metabolic.
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This invention describes a novel non-human transgenic animal (I) whose germ cells and somatic cells contain a knockout mutation in DNA encoding a 4B-BP1 (a member of eukaryotic initiation factor 4B (eIP-4B)-binding
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02-FEB-2000;
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                                                                                                                          Disclosure; Fig 7; 80pp; English
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Pred. No. 0.00013;
Mismatches 0;
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           AAB84401-15 represent 4E-binding sites. 4E-binding protein 1 (4E-BP1) is a repressor of cap-dependent translation initiation, and selectively activates apoptosis in Ras-transformed fibroblasts and eliminates Ras-induced chemoresistance. The effects of 4E-BP1 are strictly dependent on its ability to sequester the translation initiation factor elF4E, thereby preventing its assembly into an active pre-initiation complex. The specification describes a method for inducing apoptosis in a cell in which the apoptosis pathway is inhibited. The method comprises decreasing the amount of elF4E pre-initiation complex by sequestration of elF4E.
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22-AUG-2001
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UNIV MINNESOTA.
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complex by The method
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 sequestration is useful for
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Query Match

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                                                       AABB4401-15 represent 4E-binding sites. 4E-binding protein 1 (4E-BP1) is a repressor of cap-dependent translation initiation, and selectively activates apoptosis in Ras-transformed fibroblasts and eliminates Rasinduced chemoresistance. The effects of 4E-BP1 are strictly dependent on its ability to sequester the translation initiation factor elP4E, thereby preventing its assembly into an active pre-initiation complex. The specification describes a method for inducing apoptosis in a cell in which the apoptosis pathway is inhibited. The method comprises decreasing the amount of elF4F pre-initiation complex by sequestration of elF4E, thus relieving an apoptosis block. The method is useful for modulating pro-apoptotic and anti-apoptotic pathways in cells, especially in Rastransformed cells. Thus, the method is particularly useful for treating cancer. The elF4E sequestering agent, 4E-BP1 or its elF4E binding portion is useful for treating high proliferative cells
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Pred. No.
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                                                                                                                                              AABB4401-15 represent 4E-binding sites. 4E-binding protein 1 (4E-BP1) is a repressor of cap-dependent translation initiation, and selectively cactivates apoptosis in Ras-transformed fibroblasts and eliminates Ras-induced chemoresistance. The effects of 4E-BP1 are strictly dependent on its ability to sequester the translation initiation factor elf4E, thereby preventing its assembly into an active pre-initiation complex. The specification describes a method for inducing apoptosis in a cell in specification describes a method for inducing apoptosis in a cell in which the apoptosis pathway is inhibited. The method comprises decreasing the amount of elf4F pre-initiation complex by sequestration of elf4E, thus relieving an apoptosis block. The method is useful for modulating pro-apoptotic and anti-apoptotic pathways in cells, especially in Rastransformed cells. Thus, the method is particularly useful for treating cancer. The elf4E sequestering agent, 4E-BP1 or its elf4E binding portion is useful for treating high proliferative cells
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4E-binding site of a elF4GI protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Inducing apoptosis in a cell in which the apoptosis pathway is inhibited, useful for treating cancer or highly proliferative cells, comprises decreasing the amount of elf4F pre-initiation complex, relieving an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sonenberg N,
                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Fig 6;
                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                         apoptosis block.
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UNIV MINNESOTA.
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llarity 100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                           80pp;
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                                                                          Score 64; DB 4;
Pred. No. 0.00013;
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                                                               Mismatches
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RESULT 10

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ADR10076
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence represents a peptide derived from an eukaryotic Initiation Factor 4G (eIF4G) protein. The specification describes eIF4G and eIF4B binding agents, such as peptides or peptidemimetics. These binding agents are used for the induction of cell death. The binding peptides are used for inducing cell apoptosis. They are used in pharmaceutical compositions for anticancer or antitumor treatment of mammalian cells. Specifically, the peptides result in growth inhibition of, or increased cytotoxicity to tumour cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Use of eukaryotic Initiation Factor 4E (elF4E) binding agents e.g. elF4E-binding peptide (elF4E-BP) derivatives as anticancer or antitumor agents for inducing apoptosis in e.g. mammalian tumor cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Binding peptide; cell death; cell
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                                                                                                    human; oligo-capping method; diagnostic marker; gene therapy; osteoporosis; neurological disease; Alzheimer; disease; Parkinson's disease; dementia; short memory; cancer; sense or motor function; emotional reaction; fear response; posteopathic; neuroprotective; nootropic; antiparkinsonian; cy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 30 AA;
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                                                                                                                                                                                                                                                                                     Human
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                             Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KKRYDREFLLGF 12
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                                                                                                                                                                                                                                                                                  for treating neurological disease Seq 3582
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                                                                                                                     cytostatic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This invention relates to novel, isolated full length human cDNA CC molecules and the encoded proteins thereof. Specifically, it refers to CC cDNA clones obtained by an oligo-capping method, where none of these CC clones are identical to any known human mRNAs. The present invention CC describes an immunoassay to identify agonists and antagonists, as well as antibodies, antisense molecules and siRNAs that can all be used to bind CC antibodies, antisense molecules and siRNAs that can all be used to bind to and modulate expression of the CDNA molecules. As such, these CC the various diseases or morbid states. In particular, they are useful in CC gene therapy for treating osteoporosis, neurological disease, Alzhaimer's CC disease, Parkinson's disease, dementia, short memory and various cancers, as well as for maintaining equilibrium of sense or motor function, and CC treating emotional reaction, fear response and panic. Accordinally, CC they exhibit osteopathic, neuroprotective, nootropic, antiparkinsonian, CC exception and tranquiliser activities. This sequence is not given in the sequence listing of the specification but office obtained on CD-ROM from the European Patent Office, Vienna Sub-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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09-MAY-2003;
                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 903
                                                                               WO2003016475-A2
                                                                                                                                                                                                              spinal
                                                                                                                                                                                                                                         Human;
                                                                                                                                                                                                                                                                                          Human Protein Q04637, SEQ ID NO 11719.
                                                                                                                                                                                                                                                                                                                                                 29-JAN-2004
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Alzheimer's diseases,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12-FEB-2004; 2004EP-00003145
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                                                                                                                                                                                                              pain; neuronal tissue; gene therapy;
segmental nerve injury; chronic cons
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                                                                                                                                                                                     nerve
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A, Ishii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ASSOC
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2003JP-00131452.
                                                                                                                                                                                  injury;
                                                                                                                                                                                                                                                                                                                                               (first entry)
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                                                                                                                                                                                     SNI; Chung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     for treating osteoporosis, neurological diseases, Parkinson's diseases, dementia and various cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nagai K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nishikawa
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Pred. No. 0.0083;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    English
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e R;
                                                                                                                                                                                                              constriction injury; CCI;
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RESULT 13
ADO19635
ID ADO19
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AC ADO19
XC ADO19
DT 12-AU
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Human
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Theum
KW Human
KW syste
KW autoi
KW autoi
KW diabe

PRO polypeptide #282

12-AUG-2004

(first entry)

ADO19635 standard; protein; 1396 AA

Human; PRO; immune related disorder; systemic lupus erythematosus; rheumatoid arthritis; osteoarthritis; juvenile chronic arthritis; systemic sclerosis; Sjogren's syndrome; vasculitis; sarcoidosis; suctoimmune haemolytic anaemia; autoimmune thrombocytopenia; thyroi

renal disease; demyelinating

thyroiditis;

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1 KKRYDREFLLGF 12

Matches

Conservative

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Mismatches

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Gaps

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413

KKRYDREFLLGF

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that is differentially expressed in neuronal tissue of a first animal consultation which regulates the subjected to pain, a method for identifying a compound which regulates the expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a method for identifying a compound or small molecule that regulates the activity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more conjumpeptides or their antibodies. The polypucleotide or the compound that modulates its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (Chung), chronic constriction injury (CCI) and spared nerve injury (Chung), chronic constriction conjury (CCI) and spared nerve injury (Shi)) in an animal (e.g. gene conjury (CCI) and spared nerve injury (Shi)) in an animal (e.g. gene conjured that segmented is a human protein (shown in Table 2 of the specification) which is differentially expressed during pain. Note:
                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention discloses a composition comprising two or more isolated rat or human polynucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence
                                                                                          Sequence 1395 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2003-268312/26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14-AUG-2001; 2001US-0312147P.
01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-0333347P.
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                                                                                                                                 ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                         specification,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENBANK; Q04637.
                           Local
l Similarity
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BAYER AG:
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                         100.0%;
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                         Score 64;
Pred. No.
                                                                                                                                                           in electronic form directly from
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                         ; DB 7;
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                                            Length 1395;
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ADP54731
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Best Local
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Wood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       central nervous system; peripheral nervous system; demyelinating polyneuropathy; Guillain-Barre syndr chronic inflammatory demyelinating polyneuropathy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to human PRO polypeptides and the polynucleotides encoding them. The polypeptides and polynucleotides are useful for treating and diagnosing immune related disorders in mammals. The immune related disorders include systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis, systemic sclerosis, Sjogren's syndrome, vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal disease, demyelinating diseases of the central or peripheral nervous system, demyelinating polyneuropathy, Guillain-Barre syndrome and chronic inflammatory demyelinating polyneuropathy. This sequence represents a human PRO polypeptide of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel PRO polypeptide e.g., PRO69614, PRO71106, or PRO86388 useful for treating an immune related disorder such as systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2004-420067/39.
N-PSDB; ADO19634.
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                                                     human; PRO; immune related disease; inflammatory immune response; immune response stimulation; antiallergic; antianaemic; antiarthrii antiatshmatic; antithishetic; antithflammatory; antipsoriatic; antitheumatic; antithbyroid; CNS; dermatological; gastrointestinal; haemostatic; hepatotropic; immunostimulant; immunosuppressive; musc nephrotropic; neuroprotective; osteopathic; respiratory; vasotropic
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1396 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 7; SEQ ID NO 564; 1731pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              spondyloarthropathy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (GETH )
            Homo sapiens
                                                                                                                                                                  Human PRO protein sequence
                                                                                                                                                                                                18-NOV-2004 (first entry)
                                                                                                                                                                                                                                                            ADP54731 standard; protein; 1396 AA
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                                                                                                                                                                                                                                                                                                                                       413
                                                                                                                                                                                                                                                                                                                                                          1 KKRYDREFLLGF 12
                                                                                                                                                                                                                                                                                                                                                                                                   12; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
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                                                                                                                                                                                                                                                                                                                                       KKRYDREFLLGF
                                           gene
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                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%;
                                                                                                                                                                   SEQ ID
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                                                                                                                                                                                                                                                                                                                                                                                                                    Score 64;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 English.
                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                   NO:707.
                                                                                                                                                                                                                                                                                                                                                                                                                   DB 8;
                                                           immunosuppressive; muscular;
respiratory; vasotropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            syndrome;
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 1396;
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                                                                                                                      antiarthritic;
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RESULT 15 AAB18792

AAB18792 standard;

protein; 1560 AA

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413

KKRYDREFLLGF 12 KKRYDREFLLGF 424

Query Match Best Local Matches

12; ш

Conservative

0

Mismatches

Similarity

100.0%; Score 64; 100.0%; Pred. No.

; DB 8; . 0.013; 0

Length 1396;

<u>,</u>

Gaps

0

Sequence 1396 AA;

#X#X#X#X#

22-JAN-2001 AAB18792

(first

entry)

Human; ribosome recruitment protein; eIF4G1; RNA-binding protein;

recruitment protein eIF4G1

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The present invention describes an isolated PRO nucleic acid (I). Also CC described: (I) a vector comprising (II; (2) a host cell comprising the CC vector of (I); (3) a process for producing a PRO polypeptides; (4) an CC isolated PRO polypeptide; (5) a chimeric molecule comprising the CC polypeptide of (4) fused to a heterologous amino acid sequence; (6) an CC antibody which specifically binds to a polypeptide of (4); (7) a CC composition of matter comprising a polypeptide of (4), an agonist or CC antagonist of the polypeptide or an antibody that binds to the CC comprising a container, a label on the container and a composition of CC matter of (7); (9) a method of treating an immune related disease in a CC mammal; (10) a method of treating an immune related disease in a CC diagnosing an immune related disease or an inflammatory immune response CC in mammal; (12) a method of identifying a compound that inhibits or CC diagnosing an immune related disease or an inflammatory immune response CC in mammal; (12) a method of identifying a compound that inhibits or CC mimics the activity of or expression of a gene encoding a PRO polypeptide CC antiasthmatic, antidiabetic, antianimatory, antiarthritic, CC antiasthmatic, antidiabetic, antiinflammatory, antiarthritic, CC antiasthmatic, antidiabetic, antiinflammatory, antiartorintestinal, CC antinostatic, hepatotopic, CC immunostimulant, immunosuppressive, muscular, cepture of the polypeptides, compositions, kits and methods are CC useful in diagnosing and treating an immune related disease and in
erythematosus, rheumatoid arthr stimulating an immune response.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID NO 707; 3009pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New PRO polynucleotides and polypeptides, useful in useful in diagnosing and treating an immune related disease, e.g. systemic lupus erythematosus, rheumatoid arthritis, diabetes mellitus or asthma and in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29-OCT-2002; 2002US-0422472P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO2004039956-A2
                                      useful in diagnosing and treating an immune related disease and stimulating an immune response. The present sequence represents PRO protein from the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (GETH ) GENENTECH INC
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√s⊤,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Clark H,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Schoenfeld J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Williams
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М.
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Search completed: November 29, 2005, 22:52:14 Job time : 117.545 secs
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                                                                                                                                      Query Match 100.0%; Score 64; DB 3; Best Local Similarity 100.0%; Pred. No. 0.015; Matches 12; Conservative 0; Mismatches 0
                                                                                                                                                                                                                                            The present sequence represents the human ribosome recruitment protein elF4G1. The protein is used for the translational activation of genes. The elF4G1 protein is an RNA-binding protein. The protein is also used for the translation of RNA molecules containing protein binding sites, identifying RNA-binding proteins, protein-protein interactions, or inhibitors or enhancers of the interactions, providing a cell or subject with therapeutic proteins, controlling the levels of translation of the therapeutic proteins, controlling the translation and stockhometry of multiple subunit proteins, screening proteins that interact with an RNA binding site, and identifying the RNA binding sites
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New nucleic acid encoding an RNA with a coding region and protein binding sites in an adjacent 5' non-coding region for translational activation of genes using the ribosome recruitment protein eIF4G.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Fig 9A-H; 140pp; English.
                                                                                                                                                                                                                Sequence 1560 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-638139/61.
N-PSDB; AAA75835.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hentze MW, De Gregorio E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (EUMO-) EURO MOLECULAR BIOLOGY LAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08-MAR-1999;
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                                                                        569
                                                                                          1 KKRYDREFLLGF 12
                                                                      KKRYDREFLLGF 580
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                                                                                                                                                                           Length 1560;
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Minimum
Maximum
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Maximum Match 100%
Listing first 45 s
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Copyright (c) 1993 - 2005 Compugen Ltd
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ADT60579
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ABM89358
AAB11103
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A. thalia
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Claim 6; Page 31; 46pp; English.

Use of eukaryotic Initiation Factor 4E (elF4E) binding agents e.g. elF4E-binding peptide (elF4E-BP) derivatives as anticancer or antitumor agents for inducing apoptosis in e.g. mammalian tumor cells.

WPI; 2001-071386/08.

Proud CG,

Herbert TP,

Lane DP,

Fahraeus

21-JUN-1999;

99GB-00014480.

(UYDU-) UNIV DUNDEE.

The present sequence represents a binding peptide for an eukaryotic Initiation Factor 4G (eIF4G) protein. The specification describes eIF4G and eIF4E binding agents, such as peptides or peptidemimetrics. These binding agents are used for the induction of cell death. The binding peptides are used for inducing cell apoptosis. They are used in pharmaceutical compositions for anticancer or antitumor treatment of mammalian cells. Specifically, the peptides result in growth inhibition of, or increased cytotoxicity to tumour cells

Query Match

100.0%;

Score 59;

DB 4;

Length 12;

Sequence 12 AA;

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X 2 2 X	Binding peptide; cell death; cell	g pep eath;	tid ce		eukaryotic apoptosis;	tic	Initiation anticancer;	Factor 4G; eIF4G; eIF4E; ; antitumor.	
RXS	Homo sapiens. WO200078803-A2	sapiens)078803-	-A2	•					
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                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence represents a peptide derived from an eukaryotic Initiation Factor 4G (eIF4G) protein. The specification describes eIF4G and eIF4E binding agents, such as peptides or peptidemimetics. These binding agents are used for the induction of cell death. The binding peptides are used for inducing cell apoptosis. They are used in pharmaceutical compositions for anticancer or antitumor treatment of mammalian cells. Specifically, the peptides result in growth inhibition of, or increased cytotoxicity to tumour cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Use of eukaryotic Initiation Factor 4E (elF4E) binding agents e.g. binding peptide (elF4E-BP) derivatives as anticancer or antitumor \varepsilon for inducing apoptosis in e.g. mammalian tumor cells.
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                    Peptide derived from wheat eukaryotic
                                                        20-APR-2001
                                                                                            AAB31452;
                                                                                                                              AAB31452 standard; peptide; 14
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                                     09-APR-1999;
02-FEB-2000;
                                                                                                                              19-OCT-2000
                                                                                                                                                                                                                                                                                                                                                   06-AUG-2003
16-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB11102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-JUN-1999;
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                                                                                                                                                                  WO200060932-A1
                                                                                                                                                                                                     Triticum aestivum
   (UYMC-) UNIV MCGILL
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and eIF4E binding agents, such as peptides or peptidemimetics. These binding agents are used for the induction of cell death. The binding peptides are used for inducing cell apoptosis. They are used in pharmaceutical compositions for anticancer or antitumor treatment of mammalian cells. Specifically, the peptides result in growth inhibition of, or increased cytotoxicity to tumour cells. note: the peptide is biotinylated and linked to penetratin
                                                                                                                                                                                                                                                                                  Eukaryotic initiation factor; eIF4E; transgenic animal; antidiabetic; knockout mutation; 4E-BP1; glucose metabolism; fat metabolism; anorectic; drug; anti-obesity; anti-fat deposition; anti-metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Use of eukaryotic Initiation Factor 4E (elF4E) binding agents e.g. elF4E-binding peptide (elF4E-BP) derivatives as anticancer or antitumor agents for inducing apoptosis in e.g. mammalian tumor cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Binding peptide; eukaryotic Initiation Factor 4G; eIF4G; eIF4E; cell death; cell apoptosis; anticancer; antitumor.
                                                                           07-APR-2000; 2000WO-CA000388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence represents a peptide derived from an eukaryotic 
Initiation Factor 4G (eIF4G) protein. The specification describes eI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example; Fig 6; 46pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                        Wheat germ eIF-4E recognition motif peptide p82.
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12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       standard; peptide;
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99US-0128559P.
2000US-0179743P.
                                                                                                                                                                                                                                                                                                                                                                                                                                            (revised)
(first entry)
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Pred. No.
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RESULT 5
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ID AAB8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This invention describes a novel non-human transgenic animal (I) whose compared cells and somatic cells contain a knockout mutation in DNA encoding A 4E-BP1 (a member of eukaryotic initiation factor 4E (eIF-4E)-binding protein 1) shows a phenotype of an altered glucose and/or fat metabolism compared to a control animal. The products of the invention have arridiabetic and anorectic activity. The non-human transgenic animals are useful as models for the investigation of lipid and glucose metabolism. CC energy homeostasis and associated diseases. The transgenic animals are cery homeostasis and associated diseases. The transgenic animals are cery ession and/or activity of 4E-BP1 and for screening drugs to isolate therapeutic agents which are useful as anti-obesity, anti-fat deposition cd deposition disorders. The effect of the disruption of 4E-BP1 in the cknockout mice demonstrates that an alteration of 4E-BP1 in the crissue growth, glucose metabolism and weight gain in an animal. (Updated con 06-AUG-2003 to correct OS field.)
   Query Match
Best Local S
Matches 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Non-human transgenic animal useful as model for studying lipid and glucose metabolism, has germ and somatic cells containing knockout mutation in DNA encoding eukaryotic initiation factor 4E-binding protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 16
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                                                                                                                                                                                                                                                                                                          4E-binding site; 4E-binding protein; 4E-BP; 4E-BP1; chemoresistance; cap-dependent translation initiation repressor; apoptosis; translation initiation factor; elF4E; Ras; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB84407 standard; peptide; 16 AA
                                                                                                                                                                                                                  07-JUN-2001.
                                                                                                                                                                                                                                                                               Triticum
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Inducing apoptosis in a cell in which the apoptosis pathway is inhibited, useful for treating cancer or highly proliferative cells, comprises
                                               WPI; 2001-381379/40
                                                                           Sonenberg N,
                                                                                                                                                       02-DEC-1999;
                                                                                                                                                                                    01-DEC-2000; 2000WO-CA001465
                                                                                                                                                                                                                                               WO200140293-A2
                                                                                                                                                                                                                                                                                                                                                                       4E-binding site of a p82 protein.
                                                                                                         (UYMC-) UNIV MCGILL.
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                                                                              Polunavsky
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Pred. No.
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RESULT 6
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Best Local S
Matches 12
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                                                                                                                                                                                                                                                                                                                                                                                                        Plant; transgenic; cold tolerance; growth rate; drought tolerance; disease resistance; galactomannan production; heat tolerance; herbicide tolerance; lignin production; extreme osmotic condition tolerance; pathogens resistance; pest resistance; yield improvement; seed oil yield; seed protein yield.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB84401-15 represent 4E-binding sites. 4E-binding protein 1 (4E-BP1) is a repressor of cap-dependent translation initiation, and selectively
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Fig 6;
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                                                                                    New recombinant DNA constructs useful in the field of biochemistry genetics, and in particular for producing transgenic plants with in biological characteristics.
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28-APR-2003;
                                                                                                                                                                                                                                                                                                                                                                             Viridiplantae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Plant polypeptide,
                                                                                                                                                   WPI; 2004-757369/74.
                                                                                                                                                                                                                                                                                     18-DEC-2003; 2003US-00739930
                                                                                                                                                                                                                                                                                                                   28-OCT-2004.
                                                                                                                                                                                                                                                                                                                                                US2004216190-A1
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                                                                                                                                                                               Kovalic
                                                                                                                                                                                                            (KOVA/) KOVALIC D
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                                                          2; SEQ ID NO 10656; 14pp; English.
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2003US-00425115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entry)
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Pred. No. 0.00058;
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                                                                                                         improved
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The invention relates a recombinant DNA construct comprising a polynucleotide having any of 5544 nucleotide sequences (cDNAs 1-5544) and encoding a polypeptide with any of 5544 amino acid

SEQ ID NO: sequences

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RESULT 7
ADQ37031
ID ADQ37031
AC ADQ3
XX ADQ7
CC01
XX CC01
XX CC1
XX CC1
XX CC1
XX CC2
XX CC2
XX CC3
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                                                 Cooper B;
                                                                                                                                                                                                                 26-DEC-2002;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cell proliferation related polypeptide; cell proliferation; senescence;
differentiation; stress response.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cell proliferation-related polypeptide #93.
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                                                                                                                                 (SYGN ) SYNGENTA PARTICIPATIONS
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Pred. No. 0.04;
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RESULT 8
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                                                                                      New isolated nucleic acids and proteins, useful for producing transgenic plants having improved properties, e.g. tolerance to peats, herbicides, or biotic or abiotic stresses, improved nutritional value, or increased yield or proliferation.
                                                                                                                                                          N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                               rice; stress-related protein; plant maturation; plant development; plant proliferation, plant senescence; plant disease-resistance; plant stress response; transgenic plant; pest tolerance; herbicide tolerance; biotic stress tolerance; abiotic stress tolerance; improved nutritional value; increased yield; increased proliferation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rice stress-related protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADQ15701 standard; protein; 792 AA.
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                                                               Claim
                                                                                                                                                                                                                                                   26-DEC-2002; 2002US-0436564P.
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                                                                                                                                                                                                                                                                                                      22-JUL-2004
                                                                                                                                                                                                                         (SYGN ) SYNGENTA PARTICIPATIONS
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DB; ADQ15700.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       invention relates to an isolated nucleic
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Pred. No. 0.
                                                             English
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The invention comprises the amino acid and coding sequences of rice stress-related proteins. The DNA and protein sequences of the invention are useful for regulating and controlling plant maturation and development, including proliferation, senescence, disease-resistance, or

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ABMOSTATE ABMONIAN AB
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                                     CC and polypeptides. Also disclosed are vectors, expression cassettes, host cells, and plants containing such polynucleotides. Also disclosed are cc methods for using the polynucleotides and polypeptides to alter the responsiveness of a plant to abiotic stress. The invention is useful in cc agriculture. The nucleic acid is useful for determining whether a test contains the polynucleotide stress condition. It is also useful cc for selecting an agent that alters abiotic stress condition. It is also useful cc polynucleotide expression in a plant cell, and to identify a homolog or cortholog to an abiotic stress responsive polynucleotide. The nucleic acid cc molecule and the polypeptide encoded by it are useful in altering the cc responsiveness of a plant to an abiotic stress, such as cold stress, salt cc stress, osmotic stress or any of their combinations. The present sequence cc is used in the exemplification of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim
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24-AUG-2001; 2001US-0314662P.
26-SEP-2001; 2001US-0325277P.
21-NOV-2001; 2001US-0332132P.
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T, Provart
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N, Ricke
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Pred. No. 0.84
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D, Zhu T;
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                                                                                                                                                                             This invention describes a novel non-human transgenic animal (I) whose germ cells and somatic cells contain a knockout mutation in DNA encoding CC a 4E-BP1 (a member of eukaryotic initiation factor 4E (eIF-4E)-binding CC protein 1) shows a phenotype of an altered glucose and/or fat metabolism CC when compared to a control animal. The products of the invention have antidiabetic and anorectic activity. The non-human transgenic animals are CC useful as models for the investigation of lipid and glucose metabolism, CC energy homeostasis and associated diseases. The transgenic animals are CC also useful for selection and identification of modulators of the cxpression and/or activity of 4E-BP1 and for screening drugs to isolate therapeutic agents which are useful as anti-obesity, anti-fat deposition CC disorder, anti-diabetes and anti-metabolic diseases associated with fat deposition disorders. The effect of the disruption of 4E-BP1 in the kinckout mice demonstrates that an alteration of 4E-BP1 can modulate fat
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Non-human transgenic animal useful as model for studying lipid and glucose metabolism, has germ and somatic cells containing knockout mutation in DNA encoding eukaryotic initiation factor 4E-binding protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  drug; anti-obesity; anti-fat deposition; anti-metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A. thaliana eIF-4E recognition motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB11103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB11103 standard; peptide; 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sonenberg N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09-APR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Fig 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              knockout
                                                                                                         Sequence 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (UYMC-)
                                                                                                                                                            tissue growth,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2000-672657/65.
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Similarity
8; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mutation;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 initiation factor; eIF4E; station; 4E-BP1; glucose me
                                                                                                           A
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                                                                                                                                                               glucose metabolism and weight gain in an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99US-0128559P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        83.1%;
75.0%;
                            76.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 49;
Pred. No.
                            Score
Pred.
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                            No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 peptide eIF4G
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                               DB 3;
0.24;
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                                                     Length 16;
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     Indels
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문 ક

RVKYTREQLLEL RVRYSRDQLLDL 12

12

Matches

Conservative

Mismatches

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RESULT 11
AAB84408
                                                                                RESULT 12
AAG47553
                                                                                                                                                                                           Matches
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                                                                                                                                                                                                                                                                   AABB4401-15 represent 4E-binding sites. 4E-binding protein 1 (4E-BP1) is a repressor of cap-dependent translation initiation, and selectively activates apoptosis in Ras-transformed fibroblasts and eliminates Rasinduced chemoresistance. The effects of 4E-BP1 are strictly dependent on its ability to sequester the translation initiation factor elf4E, thereby preventing its assembly into an active pre-initiation complex. The specification describes a method for inducing apoptosis in a cell in which the apoptosis pathway is inhibited. The method comprises decreasing the amount of elf4E pre-initiation complex by sequestration of elf4E, thus relieving an apoptosis block. The method is useful for modulating pro-apoptotic and anti-apoptotic pathways in cells, especially in Rastransformed cells. Thus, the method is particularly useful for treating cancer. The elf4E sequestering agent, 4E-BP1 or its elf4E binding portion is useful for treating high proliferative cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Inducing apoptosis in a cell in which the apoptosis pathway is inhibited, useful for treating cancer or highly proliferative cells, comprises decreasing the amount of elF4F pre-initiation complex, relieving an apoptosis block.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI;
               18-OCT-2000
                                          AAG47553;
                                                                   AAG47553 standard;
                                                                                                                                                                                                                                               Sequence 16 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Fig 6; 80pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sonenberg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (MINU ) UNIV MINNESOTA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4E-binding site; 4E-binding protein; 4E-BP; 4E-BP1; chemoresistance; cap-dependent translation initiation repressor; apoptosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4E-binding site of a elF4G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22-AUG-2001
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RVKYTREQLLEL 12
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               (first
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                                                                  protein;
               entry)
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                                                                                                                                                                                                      76.3%;
66.7%;
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Pred. No. 0.24
4; Mismatches
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  18-JUN-1999
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16-JUN-1999;
17-JUN-1999;
18-JUN-1999;
18-JUN-1999;
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01-JUN-1999
03-JUN-1999
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07-JUN-1999
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10-JUN-1999
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24-MAY-1999;
25-MAY-1999;
27-MAY-1999;
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04-MAY-1999;
05-MAY-1999;
06-MAY-1999;
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28-APR-1999;
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14-MAY-1999
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07-MAY-1999
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06-APR-1999;
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19-MAY-1999
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19-APR-1999;
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29-MAR-1999
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09-MAR-1999
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RESULT 13
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AC AAG47
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Best Local S
Matches 8
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31-AUG-1999;
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11-SEP-1999;
13-SEP-1999;
14-SEP-1999;
22-SEP-1999;
23-SEP-1999;
24-SEP-1999;
24-SEP-1999;
25-OCT-1999;
14-OCT-1999;
                         Protein identification; signal transduction hybridisation assay; genetic mapping; gene termination sequence.
Arabidopsis thaliana
                                                                                                                                              AAG47552;
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6 RVKYTREQLLEL 187
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Similarity 66.7%;
8; Conservative
                                                                                   thaliana protein fragment SEQ ID NO: 59948.
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99US-015133P.
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99US-0154018P.
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99US-0155486P.
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                                              pathway; metabolic expression control;
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promoter;
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                                                                                                                Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                                                                                 Arabidopsis thaliana protein fragment SEQ ID NO: 59947.
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            25-FEB-2000; 2000EP-00301439
                                                                                        Arabidopsis thaliana
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99US-013421BP.
99US-013945BP.
99US-0140354P.
99US-0141284PP.
99US-01412920P.
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06-MAY-1999; 99US-00304517.
05-NOV-2001; 2001US-00985678.
                                                                 28-APR-2003; 2003US-00425114.
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3-0143542P. 3-014905P. 3-0144085P. 3-0144085P. 3-0144325P. 3-0144331P. 3-0144331P. 3-0144332P. 3-0144334P. 3-0144332P. 3-0144332P. 3-0144332P. 3-0144332P.

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Search completed: November 29, 2005, 22:52:17 Job time : 117.545 secs
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                                                                                                                                                                                                                                                                    The invention describes a recombinant DNA construct comprising a conjunct consisting of a sequence encoding an amino acid sequence or valiable in electronic form from the US patent office at the interest of the sequence encoding an amino acid sequence of the invention are also useful in physical arrays of molecules and as plant breeding markers. The recombinant DNA construct is useful for improving plant tolerance to cold, heat, drought, herbicides, extreme commotic conditions, pathogens or pests, for manipulating growth rate in plant cells by modification of the cell cycle pathway, for conferring conformation in plant disease, for producing galactomannan, constructed resistance to plant disease, for producing galactomannan, constitution of plant growth regulators, for increasing the rate of homologous crecombination in plants, for improving yield by modification of photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake corporate or providing improved plant growth and development under at least one stress condition or for modifying seed oil or protein yield and/or content. This is the amino acid sequence of a plant full length insert complypeptide that can be used in the recombinant DNA construct of the
                                                                                                                                          Query Match
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Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New recombinant DNA construct, useful for improving plant tolerance to cold, heat, drought, herbicides, extreme osmotic conditions, pathogens pests, for conferring increased resistance to plant disease, or for improving yield.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Liu J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (LIUJ/)
(ZHOU/)
(KOVA/)
(SCRE/)
(TABA/)
(CAOY/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; SEQ ID NO 37174; 15pp; English
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KOVALIC D K.

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TABASKA J E.

CAO Y.
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66.7%;
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GGDEF family prote
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ALIGNMENTS

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translation initiation factor eIF-4F isozyme form subunit p82 - wheat C;Species: Triticum sp. (wheat)
C;Date: 10-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul
C;Date: 10-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul
C;Accession: A44452
R;Allen, M.L.; Metz, A.M.; Timmer, R.T.; Rhoads, R.E.; Browning, K.S.
J. Biol. Chem. 267, 23235-23236, 1992
A;Title: Isolation and sequence of the cDNAs encoding the subunits of A;Reference number: A44452; MUID:93054655; pMID:1385417
A;Accession: A44452
                                                                                                                                                                                                                                                                                                        R;Coque, J.J.R.; Liras, P.; Martin, J.F.
EMBO J. 12, 631-639, 1993
A;Title: Genes for a beta-lactamase, a penicillin-binding protein
A;Reference number: S36188; MUID:93178438; PMID:8440253
A;Accession: S36188
                                                                                                                                                                                                                                                                                                                                                                                                         beta-lactamase (EC 3.5.2.6) I precursor - Streptomyces lactamdurans
C;Species: Streptomyces lactamdurans
C;Date: 13-Jan-1995 #sequence_revision 06-Jun-1997 #text_change 05-Oct-2004
C;Accession: S36188; S22750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT
A44452
                                                                                                                                                                                A;Cross-references: UNIPROT:Q06316; A;Note: the nucleotide sequence was C;Genetics:
                                                                                                                                                                                                                                        A;Status: nucleic acid sequence not shown; translation not A;Molecule type: DNA A;Residues: 1-302 <COQ>
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S36188
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A;Note: sequence extracted from NCBI backbone (NCBIP:1182)
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Pred. No.
    Score 40;
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T22182
hypothetical protein F44F1.7 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change
C;Accession: T22182; T23650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Glass, J.I.; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, submitted to GenBank, February 2000
A;Description: The complete sequence of Ureaplasma urealyticum: Alternate views
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              glycosyltransferase UU503 [imported] - Ureaplasma urealyticum
C;Species: Ureaplasma urealyticum
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
C;Accession: F82883
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A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A;Reference number: A84420; MUID:20083487; PMID:10617197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         probable RNA-binding protein [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
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A; Residues: 1-312 <GLA>
A; Cross-references: UNIPARC: UPI00000C1C98;
A; Experimental source: serovar 3; biovar 1
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A;Accession: F82883
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A;Gene: At2g22090
A;Gene: At2g22090
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A;Molecule type: DNA
A;Residues: 1-347 <STO>
A;Cross references: UNI
                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Reference number: A84420;
A;Accession: H84608
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7; Conservative
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Pred. No. 15;
2; Mismatches
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2; Mismatches
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C;Accession: B96501

R;Theologis, A.; Ecker, J.R.; Palm, C. Chin, C.W.; Chung, M.K.; Conn, L.; Co ansen, N.F.; Hughes, B.; Huizar, L. Nature 408, 816-820, 2000

A;Authors: Hunter, J.L.; Jenkins, J.; C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu,

hypothetical protein F2J6.12 (imported) - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Mar_2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004

C.J.; Federspiel, N.A.; Conway, A.B.; Conway, A.

iel, N.A.; Kaul, S.; White, O.; Alonso, Conway, A.R.; Creasy, T.H.; Dewar, K.;

Johnson-Hopson, C.; Khan, S.; S.X.; Liu, Z.A.; Luros, J.S.;

Khaykin, E.; Kim, C. Maiti, R.; Marziali,

B96501

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R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Mucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium A;Reference number: A33650; MUID:20512582; PMID:11058132
A;Accession: H83932
                                                                                                                                 A;Gene: BH2264
C;Superfamily: ompR protein; response regulator homology
                                                                                                                                                                                        A;Residues: 1-231 <STO>
A;Cross-references: UNIPROT:Q9KAM3; UNIPARC:UPI00000C3E63; GB:AP001514; GB:BA000004;
A;Experimental source: strain C-125
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A; Introns: 98/1; 375/1;
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                                                                                                                                                                                                                                                                                                                                                                                                    two-component response regulator BH2264 [imported] - Bacillus halodurans (strain C;Species: Bacillus halodurans
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     submitted to the EMBL Data Library, October 1996 A;Reference number: Z19527 A;Accession: T22182
                              S
                                                                                                                                                                                                                                            A; Molecule type: DNA
                                                                                                                                                                                                                                                           A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                 C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT
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                                                                                  Query Match
Best Local
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171
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                                                                 Similarity 7; Conserv
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8; Conserv
                              YSRDQLLDL 12
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YTREQLLDL 179
                                                                     Conservative
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                                                                                  64.48;
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66.7%;
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                                                                                   Score 38;
Pred. No.
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Pred. No. 39;
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                                                                     Mismatches
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Hiran

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probable acyl CoA synthetase [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: G96530
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
Nature 408, 81
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A;Accession: B96501
                                                                                                                                                                                                                       probable long-chain-fatty-acid-CoA ligase N;Alternate names: acyl CoA synthetase C;Species: Brassica napus (rape) C,Date: 21-May-1999 #sequence_revision 21-C;Accession: T07928
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A; Residues: 1-613 <STO>
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C; Superfamily:
                                                                                          A; Reference number: A; Accession: T07928
                                                                                                                                submitted to the EMBL Data Library, April A, Reference number: Z16223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Gene: F13F21.14
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A;Cross-references: UNI
                                                                                                                                                                                                  R,Fulda, M.
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;Gene: F2J6.12
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Best Local
Status: translated from Molecule type: mRNA Residues: 1-666 <FUL>
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58.3%;
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58.3%;
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Pred.
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Pred. No.
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RMSRDELIDL

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RYSRDQLLDL

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A;Title: Cloning of the gene encoding streptococcin A-FF22, a novel lantibiotic producet A;Reference number: A58598; MUID:93319301; PMID:8328813
A;Accession: T09007
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-689 <HYN>
A;Residues: 1-689 <HYN>
A;Cross-references: UNIPROT:031053; UNIPARC:UPI00000AF8A4; EMBL:AF026542; NID:g2502065; A;Experimental source: strain FF22
C;Genetics:
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C;Superf
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C;Date: 11-Jun-1999 #text_change 09-Jul-2004
C;Date: 11-Jun-1999 #text_change 09-Jul-2004
C;Accession: T09007
R;Hynes, W.L.; Ferretti, J.J.; Tagg, J.R.
Appl. Environ. Microbiol. 59, 1969-1971, 1993
Appl. Environ. Microbiol. 59, 1969-1971, 1993
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                                                                                                                                                                                                                                   R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Koloff, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.; Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein CC0846 [imported] - Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
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                                                                                                                                                     A;Residues:
                                                                                                                                                                                          A; Status: preliminary
                                                                                    A;Gene:
                                                                                                                                                                      A; Molecule type: DNA
Query Match
Best Local S
Matches 7
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;Keywords: acid-thiol ligase; coenzyme A
;100-646/Domain: acetate-CoA ligase homology <ACL>
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Best Local (
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                                                                                                                            Cross-references: UNIPROT:Q9A9W5; UNIPARC:UPI00000C71B9; GB:AE005673;
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Best Local
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6; Conserve
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  Similarity 7; Conserv
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70.0%;
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Pred. No. 49;
3; Mismatches
                        Score 37;
Pred. No.
        Mismatches
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15;
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49;
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hypothetical protein F35G12.10 - (C.Species: Caenorhabditts elegans C;Date: 15-Oct-1999 #semienca rom.
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A; Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J. A; Title: Comparative genomics of Listeria species.
A; Reference number: AB1077; MUID:21537279; PMID:11679669
A; Accession: AG1762
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C; Accession: AG1762
R; Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, R; Glaser, P.; Frangeul, G.; Duchaud, E.; Durand, L.; I Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; I T. M.; Karst, U.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Science 294, 849-852, 2001
A; Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, ok, C.; Schlueter, T.; Simose, N.; Tierrez, A.; Vazquez-Boland, J., Title: Comparative genomics of Listeria species.
A; Reference number: AB1077; MUID:21537279; PMID:11679669
A; Accession: AE1387
                                                                    RESULT 14
T21803
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A;Molecule type: DNA
A;Residues: 1-236 <GLA>
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                                                                                                                                                                                                                                                                                                                                                                                                  A;Molecule type: DNA
A;Residues: 1-236 <GLA>
A;Cross-references: UNIDROT:0927Z2; UNIDARC:UPI00000CC931; GB:AL592022; PIDN:CAC97871.1
A;Experimental source: strain Clip11262
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Science 294,
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C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001
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Best Local (
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nes 7; Conserv
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  #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
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87.5%;
                                            Caenorhabditis elegans
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Pred. No.
                                                                                                                                                                                                                                                                          Score 37; DB
Pred. No. 23;
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23;
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Dussurget, O.; Entian,
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atian, K.D.;
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Voss, H.; Wehland,
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Voss, H.; Wehland,
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Fsihi, H.
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Search completed: November 29, Job time: 20.8182 secs

2005,

23:02:32

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GGDEF family protein VC0900 [imported] - Vibrio cholerae (strain N16961 serogroup C;Species: Vibrio cholerae
C;Species: Vibrio cholerae
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C;Accession: D8265
R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sell 1, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 submitted to the EMBL Data Library, October 1994
A;Reference number: Z19473
A;Accession: T21803
A;Status: preliminary; translated from GB/EMBL/D
A;Molecule type: DNA
A;Residues: 1-301 <WIL>
                                                                                                                                                                                                                                                                                                                   A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio A;Reference number: A82035; MUID:20406833; PMID:10952301 A;Accession: D82265
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R;Chui, C.
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A;Experimental source: serogroup Ol; strain N16961; biotype El Tor
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A; Residues: 1-524 <HEI>
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                                                                                                                                                          A;Map
                                                                                                                                                                                                                                                                                                 A;Status: preliminary
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nes 7; Conserv
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                                       1 RVRYSRDQL 9
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                                                                            Similarity 6; Conserv
  RMRYSKDOM
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I.; Sellers, P.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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Eukaryotic initiation factor-like protein.
01yza sativa (japonica cultivar-group).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
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1- FUNCTION: Functions in close association with EIF4B
ATP-despendent RNA-unwinding.
-I- MISCELLANEOUS: In higher plants two isoforms of EIF4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=93054655; PubMed=1385417;
Allen M.L., Metz A.M., Timmer R.T., Rhoads R.E., Browning K.S.;
"Isolation and sequence of the CDNAs encoding the subunits of the isozyme form of wheat protein synthesis initiation factor 4F.";
J. Biol. Chem. 267:23232-23236(1992).
MEDLINE=22584437; PubMed=12684538; DOI=10.1073/pnas.0737574100; Cooper B., Clarke J., Budworth P., Kreps J., Hutchison D., Park S., Guimil S., Dunn M., Luginbuhl P., Ellero C., Goff S.A., Glazebrook J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct protein sequencing; RNA-binding.
SEQUENCE 788 AA; 86295 N
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Q84PB3;
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411-419; 448-458 AND
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                                                                                                                        NUCLEOTIDE SEQUENCE.
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SM00543; MIF4G; 1.
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Pred. No. 0.045;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 788;
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RATURE 420:316-320(2002).
EMBL; ALGO6594; CABO1628.3; -;
GO; GO:0003733; F:RNA binding;
GO; GO:0003733; F:RNA binding;
102231 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-22337377; PubMed=12447439; DOI=10.1038/nature01183; Feng Q., Zhang Y., Hao P., Wang S., Fu G., Huang Y., Li Y., Zhu J., Liu Y., Hu X., Jia P., Zhang Y., Zhao Q., Ying K., Yu S., Tang Y., Weng Q., Zhang L.S., Lu Y., Mu J., Lu Y., Zhang L.S., Yu Z., Fan D., Liu X., Lu T., Li C., Wu Y., Sun T., Lei H., Li T., Hu H., Guan J., Wu M., Zhang R., Zhou B., Chen Z., Chen L., Jin Z., Wang R., Yin H., Cai Z., Ren S., Lv G., Gu W., Zhu G., Tu Y., Jia J., Zhang Y., Chen J., Kang H., Chen X., Shao C., Sun Y., Hu Q., Zhang X., Zhang W. Wang L., Ding C., Sheng H., Gu J., Chen S., Ni L., Zhu F., Chen W., Lan L., Lai Y., Cheng Z., Gu M., Jiang J., Li J., Hong G., Xue Y., Han B.;
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GO; GO:0003723; F:RNA binding; IEA.
GO; GO:0006412; P:protein biosynthesis; IEA.
InterPro; IPR003890; IF eIF4G.
InterPro; IPR003891; IF_eIF4G_MA3.
Pfam; PF02847; MA3; 1.
Pfam; PF02844; MA3; 1.
SMART; SM00544; MA3; 1.
SMART; SM00543; MIF4G; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
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13-SEP-2005 (TrEMBLrel.
13-SEP-2005 (TrEMBLrel.
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Name=OSJNBa0029H02.9;
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; AY224450; AAU...
~~472; 1HU3.
61
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                                             1 RVRYSRDQLLDL 12
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Last annotation update)
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                                                                                                                                                                                                                    Score 52;
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RESULT 5
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RESULT OF RESULT
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                                                                             "Structural analysis of Arabidopsis thaliana chry
Sequence features of the regions of 1.367,185 bp
physically assigned P1 and TAC clones.";
DNA Res. 5:203-216(1998).

EMBL; AB013396; BAB08857.1; -; Genomic_DNA.
HSSP; O44432; 11HJ3.
GG; GG:0003723; F:RNA binding; IEA.
GG; GG:0003743; F:translation initiation factor;
GG; GO:0003743; F:translation initiation factor;
GG; GO:0003743; F:Translation initiation factor;
GG; GO:0003743; F:Translation factor;
GG; GO:0003743; F:Translation factor;
GG; GO:0003743; F:Translation factor;
GG; GO:0003743; F:Translation factor;
GG; GO:000541; MA3; 1.
SMART; SM00544; MA3; 1.
SMART; SM00544; MA3; 1.
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(Iso)4F p82-34).
Name=001004 A05.11;
Oryza sativa (japonica cultivar-group).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Vagonilophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
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05-JUL-2004
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Sasaki T., Matsumoto T., Katayose Y.;
Sasaki T., Katayose Y.;
Sasaki T., Matsumoto T., Katayose Y.;
Sasaki T., Katayose Y.;
Sasaki T., Matsumoto T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Eukaryotic initiation factor 4, eIF4-like protein.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core e
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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InterPro; IPRO03891; IF_eIF4G_MA3.
Pfam; PF02847; MA3; 1.
Pfam; PF02847; MA3; 1.
SMART; SM00544; MIF4G; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-98403884; PubMed-9734815;
MEDLINE-98403884; PubMed-9734815;
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Q9FJM7;
Q1-MAR-2001 (TrEMBLrel. 1
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9; Conserv
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780 AA;
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         factor.
751 AA;
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rel. 27, Last annotation updat
initiation factor (Iso)4F sub
              82359 MW;
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Pred. No.
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              7714D35200498882 CRC64;
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(Iso)4F subunit
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RESULT 8
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Q8H179 A
C Q8H179 T
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DT Q1-FEB-2
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GN Name-At5
OS Arabidop
OC Eukaryoto
OC Spermato
OC Gurasida
OX NCBI_Tax
RN [1]
RP NUCLEOTI
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Best Local S
Matches 8
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Matches
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GO; GO:0003743; F:translation initiation fa
GO; GO:0006412; P:protein biosynthesis; IEA
InterPro; IPR003890; IF eIF4G.
InterPro; IPR003891; IF_EIF4G_MA3.
Pfam; PF02847; MA3; 1.
Pfam; PF02847; MA3; 1.
SMART; SM00543; MIF4G; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nguyen M., Karlin-Neumann G., Southwick A., Tripp M., Miranc Palm C.J., Bowser L., Jones T., Banh, J., Carninci P., Chen Palm C., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H., Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozah Bcker J., Theologis A., Davis R.W., Shinn P., Yamada K., Shinozah Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BT002056; AAN72067.1; -; mRNA.
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update
Eukaryotic initiation factor 4, eIF4-like protein.
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QBHOTB;
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Eukaryota; Viridiplantae; Stropophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core et
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core evenosids II; Brassicales; Brassicaceae; Arabidopsis.
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QBH179;
                                                                                                                                             Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta;
                                                                                                                                                                                               Name=At5g57870;
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SEQUENCE 776 AA;
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  Southwick
                                                                     NCBI_TaxID=3702
                        NUCLEOTIDE SEQUENCE.
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Karlin-Neumann G., So
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r 4, eIF4-like protein.
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                                                                                                                            eudicots; rosids;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tracheophyta;
                                                                                                                                                       Tracheophyta;
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Chen H.,
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EMBL; BT000467; AAN17444.1; -; mRNA.

REMBL; BT000444; AAO30087.1; -; mRNA.

REMBL; BT003424; AAO30087.1; -; mRNA.

RSP; O43432; 1HU3.

GO; GO:0003723; F:RNA binding; IEA.

GO; GO:0003723; F:RNA binding; IEA.

GO; GO:0003723; F:RNA binding; IEA.

InterFro; IPR03390; IF eIF4G.

InterFro; IPR03390; IF eIF4G.

InterFro; IPR03390; IF eIF4G.

INTERFRO; IPR033891; IF eIF4G.

SMART; SM0544; MA3; 1.

Pfam; PF02847; MA3; 1.

Pfam; PF02847; MA3; 1.

SMART; SM0543; MIF4G; 1.

Initiation factor.

Initiation factor.
Yamada K., Banh J., Chan M.M., C
Deng J.M., Goldsmith A.D., Lee J
Tang C., Toriumi M., Wu H.C., Ye
Carninci P., Chen H., Cheuk R.,
Kamiya A., Karlin-Neumann G., Ke
                                                                                                                                                                                                                                                                                              Yamada K., Liu S.X., Sakano H., Phan
Goldsmith A.D., Lee J.M., Quach H.L.
Carninci P., Chen H., Cheuk R., Haya
Kamiya A., Karlin-Neumann G., Kawai
Miranda M., Narusaka M., Nguyen M.,
Seki M., Shinn P., Southwick A., Shi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
Putative eukaryotic initiation factor eIF4 (Putat
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Carninci P., Chen H., Cheuk
Deng J.M., Hayashizaki Y., H
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q93ZT6 ARATH PRELIMINARY;
Q93ZT6;
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                                                                                                                                                                                                                                           Submitted
                                                                                                                                                                                                                                                                      Theologis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=3702;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      initiation factor 4).
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Davis R.W.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUCLEOTIDE SEQUENCE.
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ii P., Chen H., Cheuk R., Chan M.M., Chang C.H., D
M., Hayashizaki Y., Hsuan V.W., Lee J.M., Ishida
N., Kim C.J., Narusaka M., Onodera C.S., Quach H.L.
I., Seki M., Shinn P., Tang C.C., Toroumi M., Wong
K., Yu G., Yuan S., Shinozaki K., Ecker J., Theol
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8; Conser
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780 AA; 85575 MW;
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Jaki Y., Heuan V.W., Lee J.M., Ishida J.
Narusaka M., Quach H.L., Sakurai T., S
Tang C.C., Toroumi M., Wallender B.K.,
Yu.G., Yuan S., Shinozaki K., Ecker J.
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   .M., Chang C.H., Chang E., Dale J.M., Lee J.M., Onodera C.S., Quach H.L., C., Yu G., Bowser L., Jones k R., Hayashizaki Y., Ishida J., Jones G., Kawai J., Kim C., Lam B., Lin J.,
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Pred. No. 19;
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hida J., Kamiya /
h H.L., Sakurai 7
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RA Calvo S., Campo K., Chang J., Coron M., RA Calvo S., Considine T., Cook A., Cooke P., Corum B., Cummo C., RA David R., Dawoe T., Degray S., Dodge S., Dooley K., Dorje P., RA David R., Dawoe T., Degray S., Dodge S., Dooley K., Dorje P., RA Dorjee K., Darris L., Duffey N., Dupes A., Elkins T., Engels R., RA Erickson J., Farina A., Faro S., Ferreira P., Fischer H., RA Fitzgerald M., Foley K., Gage D., Galagan J., Gearin G., Gnerre S., RA Fitzgerald M., Foley K., Gage D., Galagan J., Gearin G., Hafez N., Hafez N., Hagopian D., Hagos B., Hall J., Hatcher B., Heller A., Higgins H., RA Hagopian D., Hagos B., Hall J., Hatcher B., Heller A., Higgins H., RA Hagopian D., Handers T., Kamat A., Kamyssells M., Karlsson E., Kalls C., Kieu A., Kisner P., Kodira C., Kulbokas E., Labutti K., RA Lama D., Landers T., Leger J., Levins S., Lewis D., Lewis T., Lama D., Landers T., Leger J., Levins S., Lewis D., Lewis T., RA Lindblad-toh K., Jiu X., Lokyitsang T., Lokyitsang Y., Lucien O., RA Manning J., Marabella R., Maru K., Matthews C., Major J., RA Manning J., Marabella R., Maru K., Matthews C., Mauceli E., RA McGarthy M., Wcdonough S., Mcghee T., Meldrim J., Meneus L., RA Mesirov J., Mihalev A., Mihova T., Mikkelsen T., Meneus C., Nguyen C., RA Morbe N., Mguyen T., Nicol R., Nielsen C., Nizzari M., Norbu C., RA Morbe N., O'donnell P., Okoawo O., O'leary S., Omotosho B., Grani B., Parker S., Perrin D., Phunkhang P., Piqani B., RA Purcell S., Rachupka T., Ramasamy U., Rameau R., Ray V., Raymond C., RA Rattaa R., Richardson S., Rise C., Rodriguez J., Rogers J., Rogov P., RA Rutman M., Schupbach R., Seaman C., Settipalli S., Sharpe T.,
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GO; GO:0003743; F:translation initiation fa
GO; GO:0006412; P:protein biosynthesis; IEA
InterPro; IPR003890; IF eIF4G.
InterPro; IPR003891; IF_EIF4G_MA3.
Pfam; PF02847; MA3; 1.
Pfam; PF02847; MIF4G; 1.
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13-SEP-2005 (TrEMBLrel
13-SEP-2005 (TrEMBLrel
13-SEP-2005 (TrEMBLrel
Hypothetical protein.
ORFNames=UM04987.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Birren B., Nusbaum C., Abebe A., Abouelleil A., Adekoya E., Ait-zahra M., Allen N., Allen T., An P., Anderson M., Anderson S. Arachchi H., Armbruster J., Bachantsang P., Baldwin J., Barry A. Bayul T., Blitshsteyn B., Bloom T., Blye J., Boguslavskiy L., Bayul T., Boukhgalter B., Brunache A., Butler J., Calixte N., Browsky M., Boukhgalter B., Brunache A., Butler J., Calixte N.,
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Eukaryota; Fungi; Basidiomycota; Ustilaginomycetes;
Ustilaginomycetidae; Ustilaginales; Ustilaginaceae;
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RESULT 12
Q5Z5Q3 ORYSA PRELIMINARY;
ID Q5Z5Q3;
AC Q5Z5Q3;
DT 25-OCT-2004 (TrEMBLrel. 28,
DT 25-OCT-2004 (TrEMBLrel. 28,
DT 25-OCT-2004 (TrEMBLrel. 28,
DT 25-OCT-2004 (TrEMBLrel. 28,
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DE like.
GN Name=OSJNBa0077L03.22;
GN Name=OSJNBa0077L03.22;
OS Oryza sativa (japonica cult)
OC Spermatophyta; Magnoliophyta
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Matches 8
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InterPro; IPR003890; IF_eIF4G.
Pf4m; PR02854; MIF4G; 1.
SMART; SM00543; MIF4G; 1.
Hypothetical protein.
Hypothetical protein.
SEQUENCE 587 AA; 65922 MW; 06F76764B6984D52
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Schistosoma japonicum (Blood fluke).
Eukaryota; Metazoa; Platyhelminthes; Trematoda; I
Schistosomatoidea; Schistosomatidae; Schistosoma
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Q5D811;
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SEQUENCE 108 AA; 1
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     Oryza sativa (japonica cultivar-group).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
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                                                                                                                                                             (TrEMBLrel. 28, Created)
(TrEMBLrel. 28, Last sequence update)
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Pred. No. 3.5;
3; Mismatches
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Pred. No.
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TOTYZa sativa nippombare (GA3) genomic DNA, chromosome 6, BAC
TOTYZa sativa nippombare (GA3) genomic DNA, chromosome 6, BAC
Tolone.OSJNBa0077103.";
L Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AP005492; BAD62014.1; -; Genomic_DNA.
GO; GO:0003634; C:nucleus; IEA.
GO; GO:0003677; F:DNA binding; IEA.
GO; GO:0003723; F:RNA binding; IEA.
DR GO; GO:0003723; F:RNA binding; IEA.
DR GO; GO:0003723; F:RNA bindin
                                                                                                                                                                                                                                               RA Birren B., Nusbaum C., Abouelleil A., Allen N., Anderson S.,
RA Birren B., Barna N., Bastien V., Bloom T., Boguslavkiy L.,
RA Arachchi H.M., Barna N., Bastien V., Bloom T., Boguslavkiy L.,
RA Boukhgalter B., Butler J., Calvo S.E., Camarata J., Chang J.,
RA Choepel Y., Collymore A., Cook P., Cooke P., Corum B., DeArellano K.,
RA Choepel Y., Collymore A., Cook P., FitzGerald M., Gage D., Galagan J.,
RA Choepel Y., Collymore A., Cook P., FitzGerald M., Gage D., Galagan J.,
RA Erickson J., Faro S., Ferreira P., FitzGerald M., Gage D., Galagan J.,
RA Erickson J., Hagos B., Hall J., Horton L., Hulme W., Iliev I.,
RA Gardyna S., Gnerre S., Graham L., Grand-Pierre N., Hafez N.,
RA Hagopian D., Hagos B., Hall J., Horton L., Hulme W., Iliev I.,
RA Jaffe D., Johnson R., Jones C., Kamal M., Kamat A., Karatas A.,
RA Kells C., Landers T., Levine R., Lindblad-Toh K., Liu G., Lui A.,
RA Kells C., Landers T., Levine R., Lindblad-Toh K., Liu G., Lui A.,
RA Matthews C., Mauceli E., McCarthy M., Meldrim J., Meneus L.,
RA Mibova T., Menga V., Murphy T., Naylor J., Nguyen C., Nicol R.,
RA Mibova T., Menga V., Murphy T., Naylor J., Nguyen C., Nicol R.,
RA Niclsen C.B., Norbu C., O'Connor T., O'Donnell P., O'Neil D.,
RA Rachupka A., Ramasamy U., Raymond C., Retta R., Rise C., Rogov P.,
RA Roman J., Schauer S., Schupback R., Seaman S., Severy P., Smirnov S.,
RA Roman J., Schauer S., Schupback R., Seaman S., Severy P., Smirnov S.,
RA Talamas J., Tesfaye S., Theodore J., Topham K., Travers M.,
RA Wassiliev H., Venkataraman V.S., Viel R., Vo A., Wang S., Wilson B.,
RA M., Varyan D., Venkataraman V.S., Viel R., Vo A., Wang S., Wilson B.,
RA M., Varyan D., Venkataraman V.S., Viel R., Zümbek L., Zümbek L., Zödv M.,
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OSAZO2;
10-MAY-2005 (TrEMBLrel. 30, C
10-MAY-2005 (TrEMBLrel. 30, I
10-MAY-2005 (TrEMBLrel. 30, I
10-MAY-2005 (TrEMBLrel. 30, I
Hypothetical protein.
ORFNames=AN6228.2;
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Pfam; PF00642; zf-CCCH; 3.
SMART; SM00543; MIF4G; 1.
SMART; SM00356; ZnF_C3H1; 3.
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Burotiales; Trichocomaceae; Emericella.
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                                       "Genome Sequence of Aspergillus nidulans.";
Submitted (JAN 2004) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                         Wu X., Wyman D., Young G., Zainoun Lander E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUCLEOTIDE SEQUENCE.
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Last annotation update)
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Pred. No. 41;
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RESULT 15
QBY1Y7_RALSO
ID QBY1Y7;
AC QBY1Y7;
AC QBY1Y7;
DT 01-MAR-2002 (TrEMBLrel. 20, C1)
DT 01-MAR-2003 (TrEMBLrel. 25, L4)
DT 01-CT-2003 (TrEMBLrel. 25, L4)
DT 01-CT-2003 (TrEMBLrel. 25, L4)
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Q4VWT9 9 UNOC
ID Q4VWT9 13-SEP-2
DT 13-SEP-2
OC Oikopleu
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GO; GO:0003677;
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NON_TER
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seo H.C., Maeland A.D., Edvardsen R.B., Chourrout D.;
"Hypervariable and Highly Divergent Intron/Exon Organizations Chordate Oikopleura dioica.";
Submitted (MAY-2003) to the EWBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: Nuclear (By similarity).
EMBL; AY294053; AAQ63435.1; -; Genomic_DNA.
InterPro; IPR001356; Homeobox.
InterPro; IPR01287; Homeobox.
InterPro; IPR01287; Homeobox.
InterPro; IPR00047; HTH_lambrepressr.
Pfam; PF00046; Homeobox; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PR00024; HOMEOBÓX.
PRINTS; PR00031; HTHREPRESSR.
ProDom; PD000010; Homeobox; 1.
SMART; SM00389; HOX; 1.
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PROSITE; PS50829; GYF; 1.
Hypothetical protein; Nuclear protein.
SEQUENCE 1524 AA; 161671 MW; 8BF805D0D0266D
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SMART; SM00444; GYF; 1
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PROSITE; PS50071; HOMEOBOX_2; 1.
DNA-binding; Homeobox; Nuclear protein
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InterPro; IPR003169; GYF.
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Local Similarity 80.0%;
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75.0%;
  Last sequence update)
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TRANSCRIPTION REGULATOR PROTEIN.
                                                                                 Created)
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Pred. No. 93;
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Pred. No. 6.7;
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GANGE DE RESERVATION 
Search completed: November 29, 2005, 23:01:19 Job time: 118.091 secs
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R GO; GO:0003577; F:DNA binding; IEA.

R GO; GO:0000356; F:two-component response regulator activity; IEA.

R GO; GO:0000156; F:two-component response regulator activity; IEA.

R GO; GO:0000160; P:two-component signal transduction system (p. . .; IEA.

R GO; GO:0000160; P:two-component signal transduction system (p. . .; IEA.

R GO; GO:0000160; P:two-component signal transduction system (p. . .; IEA.

R GO; GO:0000160; P:two-component signal transduction system (p. . .; IEA.

R GO; GO:0000160; P:trans_reg_C.

R InterPro; IPR001789; Response_reg; I.

R Pfam; PF00072; Response_reg; I.

R PFADN; PF000329; Trans_reg_C; 1.

R ProDom; PD000329; Trans_reg_C; 1.

R ProDom; PD000329; Trans_reg_C; 1.
                                                                                                                                                                                                                                                                                                                            Matches
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Best Local
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STRAIN-GMI1000;

MEDLINE-21681879; PubMed=11823852; DOI=10.1038/415497a;

MEDLINE-21681879; PubMed=11823852; DOI=10.1038/415497a;

Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S., Salanoubat M., Choisne N., Claudel-Renard C., Cunnac S., Demange N., Chandler M., Choisne N., Claudel-Renard C., Cunnac S., Demange N., Gaspin C., Lavie M., Moisan A., Robert C., Saurin M., Schiex T., Siguier P., Thebault P., Whalen M., Wincker P., Levy M.,

Weissenbach J., Boucher C.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS50110; RESPONSE REGULATORY; 1.
Complete proteome; DNA-binding; Sensory transduction; Transcription;
Transcription regulation; Two-component regulatory system.
SEQUENCE 232 AA; 25020 MW; FB102E1671C0AA71 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ralstonia solanacearum (Pseudomonas solanacearum).
Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Burkholderiaceae; Ralstonia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nacute 15:397-302(2002).
-|-SUBCELULAR LOCATION: Cytoplasmic (By similarity).
EMBL; AL646059; CAD14078.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Genome sequence of the plant pathogen Ralstonia solanacearum.";
Nature 415:497-502(2002).
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Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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      Pred. No. 18 the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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DB seq length: 2000000000
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      protein search, using
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Match
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1: /cgn2_6/ptodata/1/iaa/5_COMB.pep:*

2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*

3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*

4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*

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US-09-621-976-7566
US-08-481-435-13
US-08-481-435-13
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US-08-481-435-7
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US-08-481-435-7
US-08-481-435-8
US-09-489-039A-12429
US-09-489-039A-12429
US-09-252-991A-30457
US-09-252-991A-19848
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34.645 Million cell updates/sec
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12429, A
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US-08-751-344B-5 US-08-751-344B-5 ; Sequence 5, Application US/08751344B ; Patent No. 6210960 ; GENERAL INFORMATION: APPLICANT: Habener M.D., Joel F. APPLICANT: Miller Ph.D., Christopher P. TITLE OF INVENTION: NOVEL TRANSCRIPTION FACTOR AND USES TITLE OF INVENTION: THEREFOR NUMBER OF SEQUENCES: 29 CORRESPONDENCE ADDRESS: ADDRESSEE: Banner & Witcoff, Ltd. STREET: One Financial Center CITY: Boston STATE: MA COUNTRY: US ZIP: 02111 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS	Query Match Best Local Similarity 66.7%; Score 40; DB 2; Length 117; Best Local Similarity 66.7%; Pred. No. 3.8; Matches 8; Conservative 2; Mismatches 2; Indels 0; C Qy 1 RVRYSRDQLLDL 12	RESULT 1 US-09-621-976-7566 US-09-621-976-7566 Sequence 7566, Application US/09621976 Fatent No. 6639063 GENERAL INFORMATION: APPLICANT: Dumas Milne Edwards, J.B. APPLICANT: Jobert, S. APPLICANT: Jobert, S. APPLICANT: Giordano, J.Y. FILLE REFERIOE: GENSET.054PR2 CURRENT APPLICATION NUMBER: US/09/621,976 CURRENT APPLICATION NUMBER: US/09/621,976 CURRENT FILING DATE: 2000-07-21 NUMBER OF SEQ ID NOS: 19335 SOFTWARE: Patent.pm SEQ ID NO 7566 LENGTH: 117 TYEE: PRT ORGANISM: Homo sapiens US-09-621-976-7566	ALIGNMENTS	28 34 57.6 61 1 US-08-757-316C-30 Sequence 3 29 34 57.6 105 2 US-09-583-110-3678 Sequence 3 30 34 57.6 106 2 US-09-621-976-6229 Sequence 3 31 34 57.6 106 2 US-09-513-9996-8160 Sequence 3 32 34 57.6 109 2 US-09-513-9996-8160 Sequence 3 33 34 57.6 113 2 US-09-640-211A-631 Sequence 3 34 57.6 129 2 US-09-640-211A-631 Sequence 3 35 34 57.6 129 2 US-09-983-110-3614 Sequence 3 36 34 57.6 129 2 US-09-910-72112 Sequence 1 37 34 57.6 272 2 US-09-538-577-11 Sequence 1 38 34 57.6 283 1 US-08-583-672-2 Sequence 2 39 34 57.6 283 1 US-08-583-672-2 Sequence 2 39 34 57.6 283 1 US-08-583-672-2 Sequence 2 40 34 57.6 283 1 US-08-751-344B-2 Sequence 3 41 34 57.6 284 2 US-08-784-582-6 Sequence 6 42 34 57.6 284 2 US-08-784-582-6 Sequence 6 43 34 57.6 284 2 US-08-785-271-6 Sequence 6 44 34 57.6 284 2 US-08-785-271-6 Sequence 6 45 34 57.6 284 2 US-08-785-271-6 Sequence 6 46 34 57.6 284 2 US-08-785-271-6 Sequence 6 47 34 57.6 284 2 US-08-785-271-6 Sequence 6 48 34 57.6 284 2 US-08-785-271-6 Sequence 6 49 34 57.6 284 2 US-08-785-271-6 Sequence 6 49 34 57.6 284 2 US-08-785-271-6 Sequence 6 40 34 57.6 284 2 US-08-785-271-6 Sequence 6 41 34 57.6 284 2 US-08-785-271-6 Sequence 6 42 34 57.6 284 2 US-08-785-271-6 Sequence 6 43 34 57.6 284 2 US-08-785-271-6 Sequence 6 45 34 57.6 284 2 US-08-785-271-6 Sequence 6 47 34 57.6 284 2 US-08-785-271-6 Sequence 6 48 34 57.6 284 2 US-08-785-271-6 Sequence 6 49 34 57.6 284 2 US-08-785-271-6 Sequence 6 49 34 57.6 284 2 US-08-785-271-6 Sequence 6 49 34 57.6 284 2 US-08-785-271-6 Sequence 6 40 34 57.6 284 2 US-08-785-271-6 Sequence 6 41 34 57.6 284 2 US-08-785-271-6 Sequence 6 42 34 57.6 284 2 US-08-785-271-6 Sequence 6 43 34 57.6 284 2 US-08-785-271-6 Sequence 6
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US-08-481-435-13
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Best Local Similarity 66.7%;
Matches 8; Conservative
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APPLICANT: Balgane
APPLICANT: Town,
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HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: in
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NFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
REFERENCE/DOCKET NUMBER: 35,372
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 819-8783
TELEPROV (212) 819-8783
                                                                                                                                                                                                 APPLICATION NUMBER: IN 580/MAS/94
FILING DATE: 01-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 9404072-2
FILING DATE: 24-NOV-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/481,435
FILING DATE: 10-JUL-1995
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REFERENCE/DOCKET NUMBER: 97
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 345-9100
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APPLICATION NUMBER: 08/
FILING DATE: 23-Feb-199
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 11. New York
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: No. 6027906el Polypeptides NUMBER OF SEQUENCES: 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: United States ZIP: 10036-2787
                                                                                                                                  NAME: Sterner, Richard J. REGISTRATION NUMBER: 35,3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/751,344B
FILING DATE: 19-No. 6210960-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE:
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mino acid
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Town, Christine
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Pred. No. 2.8;
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Best Local Similarity 60.0%;
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 12,
                                                                                                                                            TELEPHONE: (212) 819-8783
TELEFAX: (212) 354-8113
INFORMATION FOR SEQ ID NO: 12
SEQUENCE CHARACTERISTICS:
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                              MOLECULE TYPE: F
ORIGINAL SOURCE:
ORGANISM: Esch
                                                                                                                                                                                                                                                                                                         FILING DATE: 01-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 94
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ORIGINAL SOURCE:
ORGANISM: ESC
                                                                                                                                                                                                                              FILING DATE: 24-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Sterner, Richard J.
REGISTRATION NUMBER: 35,372
REFERENCE/DOCKET NUMBER: 110
                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: IN 580/MAS/94
                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatil
                  IMMEDIATE SOURCE:
                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: White & Case
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                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: New York
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                                                                                                  STRANDEDNESS
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                                                                                                               TYPE: amino acid
                                                                                   OPOLOGY:
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                                                                                                                                ENGTH:
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PARC 0593
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Town, Christine
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   truncated soluble PBP 1B
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Pred. No. 20;
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Length 532;

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RESULT 6
US-09-538-092-183
; Sequence 183, Application US/09538092
; Patent No. 6753314
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Best Local Similarity
6; Conserv
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                                                                                                                                                             Matches
                                                                                                                                                                          Query Match
Best Local 9
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FILING DATE: 01-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 9404072-2
FILING DATE: 24-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Sterner, Richard J.
REGISTRATION NUMBER: 35,372
REFERENCE/DOCKET NUMBER: 1103326-151
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 819-883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compartible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, V
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/481,435
FILING DATE: 10-UUL-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (212) 354-8113
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 553 amino acids
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                                                                                                                                                                                                                                                                                    MOLECULE TYPE: peptide ORIGINAL SOURCE:
                                                                                                                                                                                                                                                     ORGANISM: E8Ch
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
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                                                                                                                                                        l Similarity
6; Conserve
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                                                                                                                             3 RYSRDQLLDL 12
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                                                                                                                                                                            62.7%;
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Best Local Similarity
Griches 6; Conserva
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SOFTWARE: CuraPatSeqFormatter Version 0.9
SEQ ID NO 183
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                                                                            COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/481,435
FILING DATE: 10-UUL-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IN 580/MAS/94
FILING DATE: 01-UUL-1994
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: SE 9404072-2
FILING DATE: 24-NOV-1994
ATTORNEY/AGENT INFORWATION:
NAME: Sterner, Richard J.
NAME: Sterner, Richard J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILE REFERENCE: 15966-542
CURRENT APPLICATION NUMBER: US/09/538,092
CURRENT FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: 60/127,352
PRIOR FILING DATE: 1999-04-01
PRIOR APPLICATION NUMBER: 60/178,965
PRIOR APPLICATION NUMBER: 60/178,965
PRIOR APPLICATION NUMBER: 60/178,965
PRIOR FILING DATE: 2000-02-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Giot, Loic APPLICANT: Mansfield,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Protein-Protein Complexes and Method of Using
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Saccharomyces cerevisiae
FEATURE:
FEATURE:
NAME/KEY: misc_feature
LOCATION: (0)...(0)
OTHER INFORMATION: Polypeptide Accession Number YDR292C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 621
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Balganesh, Tanj
APPLICANT: Town, Christine
TITLE OF INVENTION: No. 60
                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                    RELECOMMUNICATION INFORMATION:
                                      NAME: Sterner, Richard of REGISTRATION NUMBER: 35.
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET:
TELEPHONE:
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5. 6027906
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(212) 819-8783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    No. 6027906el Polypeptides
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54.5%;
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                                             103326-151
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INFORMATION FOR SEQ ID NO:

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US-08-481-435-9
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                                                                                    Query Match
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Patent No. 6027906
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                                                          Matches
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APPLICANT: Balgan
APPLICANT: Town,
                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: IN 580
FILING DATE: 01-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 940
FILING DATE: 24-NOV-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 10030-2...
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy (
MEDIUM TYPE: TOPM PC com
                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFFWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/481,435 FILING DATE: 10-JUL-1995 CLASSIFICATION: 435 PRIOR APPLICATION DATA:
APPLICATION NUMBER: IN 580/MAS/94
                                                                                                                               IMMEDIATE SOURCE:
CLONE: pARC046
                                                                                                                                                                          MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                          TELEPHONE: (212) 819-8783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: LALL STREET: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: No. 6027906el Polypeptides
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Local Similarity 60.0%;
hes 6; Conservative
                                                                                                                                                                                                                                                                                                                                       NAME: Sterner, Richard J.
REGISTRATION NUMBER: 35,372
REFERENCE/DOCKET NUMBER: 1103326-151
                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                            ORGANISM:
                                                                                                                                                                                                                                                                                               TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
                                                                                                                                                                                                                   STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: United States ZIP: 10036-2787
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                                                                                                                                                                                                          COPOLOGY:
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 292
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RYSKDRILEL 301
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                                                                                                                                                                                                                                                                                               (212)
                                                          Conservative
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                                                                                                                                                                                                                                                                                9:
                                                                      Score 37; DB 2; Length 836; Pred. No. 1.2e+02;
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Pred. No. 1.2e+02;
                                                          Mismatches
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                                                                                                                                    RESULT 10
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                 Sequence 8, Application US/08481435
PATENT NO. 6027906
GENERAL INFORMATION:
APPLICANT: Balganesh, Tanjore S
APPLICANT: Town, Christine
TITLE OF INVENTION: No. 60279066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 7, Application Patent No. 6027906
                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                    Query Match
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FILING DATE: 01-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 9404072-2
FILING DATE: 24-MOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Sterner, Richard J.
REGISTRATION NUMBER: 35,372
REGISTRATION NUMBER: 35,372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (212) 819-8783
TELEFAX: (212) 354-8113
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
TITLE OF INVENTION: No. 6027906el Polypeptides NUMBER OF SEQUENCES: 42
                                                                                                                                                                                                                                                                                                                                                   IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 11
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0.
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APPLICANT: Town, Christine
TITLE OF INVENTION: No. 6027906
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 10
CLASSIFICATION:
                                                                                                                                                                                                                                                                    Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     YPE: amino acid
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CORRESPONDENCE ADDRESS:
ADDRESSEE: White & Case

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1155 Avenue of the Americas

STATE: New COUNTRY: United S COUNTRY: United S ZIP: 10036-2787

New York

COMPUTER READABLE FORM: MEDIUM TYPE: Floppy

Floppy disk

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Best Local Similarity
Thes 6; Conserve
                 Query Match
Best Local Similarity
Thes 6; Conserve
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                                                                                                           ; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-12429
                                                                                                                                                         Sequence 12429, Application US/09489039A

Patent No. 6510836

GENERAL INFORMATION:
APPLICANT: GATY Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS

PILE REFERENCE: 2709.2004001

CURRENT APPLICATION NUMBER: US/09/489,039A

CURRENT FILING DATE: 2000-01-27

PRIOR APPLICATION NUMBER: US 60/117,747

PRIOR APPLICATION NUMBER: US 60/117,747

PRIOR OF SEQ ID NOS: 14342

SEQ ID NO 12429

LENCTH: 855

TYPEN: DEPT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Sterner, Richard J.

REGISTRATION NUMBER: 35,372
REFERENCE/DOCKET NUMBER: 1103326-151
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 819-8783
TELEPHONE: (212) 819-8783
TELEPAX: (212) 354-8113
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PILING DATE: 01-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 940
PILING DATE: 24-NOV-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIA RE-BASE #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/481,435
FILING DATE: 10-UUL-1995
CLASSIFICATION: 435
CLASSIFICATION: 435
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ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: IN 580/MAS/94
FILING DATE: 01-JUL-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Escherichia coli
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
TOPOLOGY: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             300 RYSKDRILEL 309
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 3 RYSRDQLLDL 12
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                                   Conservative
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                                                      62.7%;
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                                   4; Mismatches
                                                      Score 37; DB 2;
Pred. No. 1.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 37; DB 2;
Pred. No. 1.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                      0
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                                      Gaps
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SOFTWARE: Microsoft Office 97
SEQ ID NO 42
LENGTH: 259
TYPE: PRT
ORGANISM: Triticum aestivum
US-09-452-239-42
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US-09-252-991A-30457
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US-09-452-239-42
                                                                                                RESULT 14
US-09-252-991A-28689
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APPLICANT: Rafalski, Antoni J.
APPLICANT: Fader, Gary M.
APPLICANT: Caboon, Rebecca E.
APPLICANT: CAboon, Rebecca E.
TITLE OF INVENTION: Plant Caffeoyl-CoA O-Methyltransferase
FILE REFERENCE: BB1284 US NA
CURRENT APPLICATION NUMBER: US/09/452,239
CURRENT FILING DATE: 1999-12-01
EARLIER APPLICATION NUMBER: 60/110,594
EARLIER FILING DATE: 1998-December-02
                Sequence 28689, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
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Best Local Similarity
Matches 7; Conserv
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SEQ ID NO 30457
LENGTH: 419
TYPE: PRT
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Best Local
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CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
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APPLICANT: Marc J. Rubenfield et al. TITLE OF INVENTION: NUCLEIC ACID AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
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Local Similarity 100.0%; Pred. No.
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Sequence 1988, Application US/09252991A

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US-09-252-991A-19888
Search completed: November 29, Job time: 28.6364 secs
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Best Local Similarity 63.6%; Pred. No. 2.2e+02;
Matches 7; Conservative 2; Mismatches 2; Indels
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RESULT 2 US-10-739-930-10656

Sequence 10656, Application US/10739930
Publication No. US20040216190A1
Publication No. US20040216190A1
GENERAL INFORMATION:
APPLICANT: KOVAlic, David K.
TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH TITLE OF INVENTION: PLANTS AND USES THEREOF FOR PLANT IMPROVEMENT FILE REFERENCE: 38-21(53377)B
CURRENT APPLICATION NUMBER: US/10/739,930
CURRENT APPLICATION NUMBER: US/10/739,930
CURRENT FILING DATE: 2003-12-18
NUMBER OF SEQ ID NOS: 11088
SEQ ID NO 10656

Query Match Best Local Matches 1	NESULT 1 US-09-973-473-13 ; Sequence 13, Applica ; publication No. US20 ; GENERAL INFORMATION; ; APPLICANT: SONENBER APPLICANT: TREMBLA APPLICANT: TRUKING ; TITLE OF INVENTION; TITLE OF INVENTION; TITLE OF INVENTION; FILE REFERENCE: 514 CURRENT APPLICATION CURRENT FILING DATE: PRIOR APPLICATION N PRIOR FILING DATE: PRIOR PR		0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
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Similarity 2; Conservat	Ce 13, Application US/09973473 ation No. US20030041341A1 L INFORMATION: CANT: SONENBERG, Nahum CANT: TREMBLAY, Michel CANT: TREMBLAY, Michel CANT: TREMBLAY, MICHEL OF INVENTION: NON-HUMAN TRANS OF INVENTION: SOMATIC CELLS OF INVENTION: BENCODING 4E-BE REPERENCE: 514012000400 NIT APPLICATION NUMBER: US/09/5 NIT EILING DATE: 2000-04-07 APPLICATION NUMBER: PCT/CA00/ FILING DATE: 1999-04-09 FILING DATE: 1999-04-09 FILING DATE: 2000-02-02 FILING DATE: 2000-03-03		62.77 62.77 62.77 62.77 62.77 62.77 62.77
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Score 59; DB 3; Le Pred. No. 0.0012; 0; Mismatches 0;	OKO OKO NSGENIC ANIMAL WHOSE S CONTAIN A KNOCKOUT BP1 /973,473 /0/00388 559 743	ALIGNMENTS	US-10-369-493-11354 US-10-282-122A-55450 US-10-489-034-2 US-10-282-122A-77741 US-10-282-122A-75215 US-10-282-122A-75215 US-10-282-122A-56420 US-10-282-122A-56420 US-10-282-122A-56016 US-10-282-122A-56016 US-10-12-82-122A-50016 US-10-13-85-122A-3568 US-10-179-543-23568 US-10-179-543-23568 US-11-037-143-858 US-11-037-143-858 US-11-037-143-858 US-11-037-143-858 US-11-335-977-8591 US-10-335-977-8591
ngth 16; Indels 0; Gaps	GERM CELLS AND MUTATION IN DNA		Sequence 11354 Sequence 55450 Sequence 2, App Sequence 1, App Sequence 77741 Sequence 10039 Sequence 56420 Sequence 60016 Sequence 60016 Sequence 60016 Sequence 33568 Sequence 3358 Sequence 3347, Sequence 13188 Sequence 13188 Sequence 13188 Sequence 8591, Sequence 8591,
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                NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 38015
LENGTH: 148
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SEQ ID NO 239945
LENGTH: 775
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                                                                    APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21(53535)B
CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT FILING DATE: 2004-01-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: La ROBA Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5323)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
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NAME/KEY: unsure
LOCATION: (1)..(784)
OTHER INFORMATION: unsure at all Xaa locations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: unsure
LOCATION: (1)..(775)
OTHER INFORMATION: unsure
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: Clone ID: PAT_MRT3847_58696C.1.pep
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Local Similarity 100.0%;
hes 12; Conservation
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91.7%;
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Pred. No. 0.88;
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US-10-767-701-38015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: Clone ID: MRT4577_135478C.1.pep US-10-425-115-223562
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            TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERENCE: 38-21(53221)B CURRENT APPLICATION NUMBER: US/10/437,963 CURRENT FILING DATE: 2003-05-14 NUMBER OF SEQ ID NOS: 204966 SEQ ID NO 148037 LENGTH: 752 TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 223562
LENGTH: 234
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Publication No. US20040214272A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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Best Local Similarity 83.3%;
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APPLICANT:
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APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(53222)B
                                                                                                                                                                                                                                          APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yongwei
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LOCATION: (1)..(234)
OTHER INFORMATION: unsure at all Xaa locations
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ORGANISM: Zea mays
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ORGANISM: Oryza sativa
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Wu, Wei
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                                                                                                                                                                                         Barbazuk, Brad
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Pred. No.
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Pred. No. 0.37;
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1.23;
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RESULT 7
US-10-425-115-294192
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; OTHER INFORMATION: Clone ID: PAT_MRT4530_48508C.1.pep
US-10-437-963-148037
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APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules an
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(53222)8
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILMS DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 294192
LENGTH: 785
TYPE: PRT
ORGANISM: Zea mays
                                ; OTHER INFORMATION: Clone ID: PAT_MRT3847_58697C.1.pep
US-10-424-599-239946
                                                                                                                   APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Plants and Wolecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5322)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 239946
LENGTH: 775
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Best Local S
Matches 10
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Best Local Similarity 83:
Matches 10; Conservative
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Query Match
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NAME/KEY: unsure

LOCATION: (1)...(785)

OTHER INFORMATION: unsure at all Xaa locations
                                                                    ORGANISM: Glycine max FEATURE:
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83.3%;
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Pred. No. 1.
 Score 50;
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 DB 4;
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Length 775;
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US-09-973-473-14
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US-10-424-599-231391
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                                                                                                                ; TYPE: PRT ; ORGANISM: Arabidopsis thaliana US-09-973-473-14
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SEQ ID NO 231391
LENCTH: 789
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Publication No. US20040031072A1
GENERAL INFORMATION:
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Matches 10; Conservative
                                                                                                                                                                      SEQ ID NO 14
LENGTH: 16
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                                    Query Match
Best Local Similarity
Matches 8; Conserv
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Best Local Similarity
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TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(33223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
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APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: SONENBERG, Nahum
APPLICANT: TREMBLAY, MICHE!
APPLICANT: TSUKIAYAMA-KOHARA, KYOKO
TITLE OF INVENTION: NON-HUMAN TRANSCENIC ANIMAL WHOSE GERM CELLS AND
TITLE OF INVENTION: SOMATIC CELLS CONTAIN A KNOCKOUT MUTATION IN DNA
TITLE OF INVENTION: ENCODING 4E-BP1
                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: PCT/CA00/00388
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: 60/128,559
PRIOR FILING DATE: 1999-04-09
PRIOR APPLICATION NUMBER: 60/179,743
PRIOR FILING DATE: 2000-02-02
                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/973,473
CURRENT FILING DATE: 2001-10-03
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ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_50969C.l.pep
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                                        Conservative
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75.0%;
                                                          76.3%; Score 45; D 66.7%; Pred. No. 0.
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                                                            DB 3;
0.39;
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                                                                            Length 16;
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TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION UNMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 199348
LENCTH: 719
TYPE: DDT
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; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_70754C.1.pep
US-10-437-963-172637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               밁
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US-10-437-963-199348
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                                                 Best Local Similarity 66.7%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
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SEQ ID NO 172637
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Best Local
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APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5321)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-55-14
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                                                                                                                                                                           TYPE: PRT
ORGANISM: Oryza sativa
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ENGTH:
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                     RVRYSRDQLLDL 12
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                                                             Mismatches
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Pred. No. 50;
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                                                                                                 DB 4; Length 719;
                                                           2; Indels
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RESULT 15
US-10-424-599-156877
; Sequence 156877, Application US/10424599
; Publication No. US20040031072A1
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US-10-424-599-269495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 13
US-10-424-599-269495
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Publication No. US20040031072A1

GENERAL INFORMATION:

APPLICANT: La Rosa Thomas J

APPLICANT: Kovalic David K

APPLICANT: Chou Yihua

APPLICANT: Chou Yihua

APPLICANT: Cor Yongwei

TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(5322)B

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 285684

SEQ ID NO 269495

LENGTH: 177

TUTNE OF SEC INOS: 285684
                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
                                                                                                                                                                                                                                          APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 37174
LENGTH: 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 37174, Application US/10425114 Publication No. US20040034888A1 GENERAL INFORMATION:
                                                                         Matches
                                                                     Best Local Similarity
Matches 8; Conserv
                                                                                                           Query Match
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ORGANISM: Glycine
                                                                                                                                                                  OTHER INFORMATION: Clone ID: 700866653_FLI.pep
                                                                                                                                                                                      ORGANISM: Glycine max FEATURE:
                                                                                                                                                                                                                              TYPE: PRT
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363
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                                 1 RVRYSRDQLLDL 12
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8; Conserv
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RLKYSRDELLAL 374
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80.0%;
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66.7%;
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                                                                                         Score 42; DB 4; Length 397; Pred. No. 40;
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Pred. No.
                                                                         Mismatches
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GENERAL INFORMATION:
APPLICANT: La Roba Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
CURRENT FILING DATE: 2003-04-28
UNMBER OF SEQ ID NOS: 285684
SEQ ID NO 156877
LENGTH: 576
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
NAME/KEY: Unsure
COCATION: (1)..(576)
OTHER INFORMATION: unsure at all Xaa locations
FEATURE:
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_112682C.1.pep
US-10-424-599-156877
Search completed: November 29, 2005, 23:10:27 Job time: 94.5455 secs
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                                                                                                                                                                                                                         Query Match 71.2%; Score 42; DB 4; Length 576; Best Local Similarity 66.7%; Pred. No. 59; Matches 8; Conservative 3; Mismatches 1; Indels
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542 RLKYSRDELLAL 553
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Result
No.
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Maximum DB
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Perfect score:
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Maximum Match 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Searched:
    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                 Score
    seq length: 0
seq length: 2000000000
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1: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*

2: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*

3: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*

4: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*

5: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*

6: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*

7: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*

8: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
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59
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Gapop 10.0 , Gapext 0.5
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12.124 Million cell updates/sec
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    Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                 Length DB
    US-10-467-962B-93

US-11-0485-517-127

US-11-054-515-13040

US-11-054-515-13646

US-10-93-626-1406

US-10-93-626-1712

US-10-131-826A-120

US-10-131-826A-120

US-10-131-826A-120

US-10-131-826A-120

US-10-131-826A-20

US-10-131-826A-20

US-10-131-826A-219

US-10-793-626-6192

US-10-793-626-1192

US-10-858-730-117

US-10-821-234-1195

US-11-02-762-64

US-11-074-176-148

US-11-051-869-11

US-10-93-626-3136

US-11-074-176-204
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Sequence 93, Appl
Sequence 127, Appl
Sequence 17, Appl
Sequence 136, Ap
Sequence 1406, Ap
Sequence 1154, Ap
Sequence 1154, Ap
Sequence 1172, Ap
Sequence 118, App
Sequence 20, Appl
Sequence 2128, Ap
Sequence 2128, Ap
Sequence 117, App
Sequence 118, App
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RESULT 2 US-10-48 Sequen Sequen APPLI APPLI APPLI APPLI APPLI CURRE CURRE PRIOR PRIOR	Query M Best Lo Matches Matches Qy	RESULT 1 US-10-467-962E US-1		0 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2
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-517-127 tion No. US2005025629 INFORMATION: ANT: University of Sh ANT: Poster, Simon ANT: Mondo, James OF INVENTION: Antigen EFERENCE: P100629W0 T APPLICATION NUMBER: T FILING DATE: 2004- APPLICATION NUMBER: G FILING DATE: 2011-08- FILING DATE: 2001-08- FILING DAT	imilarity; Conservat; Conservat RVRYSRDQLLDL : : RVKYYRDYLVQL			44444444444444444444444444444444444444
of Since Inc. of	59.3 ive 12 433	a 2237 1-CB 75		10067 7 11092 7 11227 1 11400 1 11158 1 1170 1 1170 1 1306 7 306 7 306 7 306 1 306 1 307 1 4420 1 44
US/10485517 \$299A1 Sheffield sherfield ncorporated n genic Polypeptides BR: US/10/485,517 04-02-02 1 GB 0118825.9 1 GB 0200349.9	%; Score 35; DB 1; Le %; Pred. No. 7.3; 2; Mismatches 3;	7962B ion of Herbicidally 10/467,962B 4	ALIGNMENTS	US/11/062 US/11/062 US-10-793-626-96 US-10-858-730-70 US-10-858-730-71 US-10-867-295-52 US-10-667-295-52 US-11-053-076-80 7 US-11-053-076-80 7 US-11-073-626-436 US-10-793-626-436 US-10-821-234-1001 US-10-793-626-3300 US-10-793-626-3300 US-10-793-626-296 US-10-793-626-296 US-10-793-626-296 US-10-793-626-296 US-10-131-826-72 US-10-131-826-72 US-11-082-389-392 US-11-082-389-392
	Length 495; ; Indels 0; Gaps	Active Substances		Sequence 3, Appli Sequence 6, Appli Sequence 96, Appl Sequence 1045, Ap Sequence 70, Appl Sequence 71, Appl Sequence 62, Appl Sequence 1022, Ap Sequence 1022, Ap Sequence 436, Appli Sequence 40, Appli Sequence 41, Appli Sequence 3300, Ap Sequence 2996, Ap Sequence 2896, Ap Sequence 52, Appl Sequence 52, Appl Sequence 52, Appl Sequence 92, Appl Sequence 390, App Sequence 390, App

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TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REFERENCE: PF523P3
CURRENT APPLICATION NUMBER: US/11/054,515
CURRENT FILING DATE: 2005-02-10
PRIOR APPLICATION NUMBER: 60/543,296
PRIOR TILING DATE: 2004-06-11
PRIOR APPLICATION NUMBER: 60/580,347
PRIOR APPLICATION NUMBER: 60/580,347
PRIOR APPLICATION NUMBER: 10/293,418
PRIOR FILING DATE: 2002-11-14
PRIOR PRIOR PRIOR DATE: 2002-11-14
PRIOR APPLICATION NUMBER: 60/331,469
PRIOR APPLICATION NUMBER: 60/340,817
PRIOR PRIOR PRIOR DATE: 2001-06-15
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; NUMBER OF SEQ ID NOS: 424
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 127
; LENGTH: 1263
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-485-517-127
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US-11-061-869-17
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SEQ ID NO 17
LENGTH: 396
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 3040, Application US/11054515 Publication No. US20050255532A1
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Best Local &
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TITLE OF INVENTION: METHODS AND COMPOSITIONS
FILE REFERENCE: CIET-P01-080
CURRENT APPLICATION NUMBER: US/11/061,869
CURRENT FILING DATE: 2005-02-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 60/168,112
PRIOR FILING DATE: 1999-11-30
NUMBER OF SEQ ID NOS: 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US/09/724,964
PRIOR FILING DATE: 2000-11-28
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nes 7; Conserv
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Similarity 58.3%;
7; Conservation
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77.8%;
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Pred. No. 21;
2; Mismatches
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Pred. No.
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PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PREMAINING PATOR APPLICATION data removed - involved of Seq ID NOS: 3247
SEQ ID NO 3040
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                                                                                                                                            ; ORGANISM: Homo sapiens US-11-054-515-1636
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Sequence 1636, Application US/11054515
Publication No. US20050255532A1
GENERAL INFORMATION:
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NUMBER OF SEQ ID NOS: 3247
SEQ ID NO 1636
LENGTH: 253
                                                                        Matches
                                                                                                        Query Match
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Best Local Similarity
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PRIOR FILING DATE: 2004-06-18
PRIOR APPLICATION NUMBER: 10/293,418
PRIOR FILING DATE: 2002-11-14
PRIOR APPLICATION NUMBER: 60/331,469
PRIOR FILING DATE: 2001-11-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/11/054,515
CURRENT FILING DATE: 2005-02-10
PRIOR APPLICATION NUMBER: 60/543,296
PRIOR FILING DATE: 2004-02-11
PRIOR FILING DATE: 2004-02-11
                                                                                                                                                                              LENGTH: 25
TYPE: PRT
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PRIOR FILING DATE: 2001-05-25
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PRIOR APPLICATION NUMBER: 09/880,748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
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                                                                    Local Similarity nes 6; Conserv
                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 60/240,816
                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 60/276,248 FILING DATE: 2001-03-16
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                                  4 YSRDQLLD 11
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YWRDELLD 115
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75.0%;
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Pred. No.
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Pred. No. 1
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RESULT 6 US-10-793-626-1406 ; Sequence 1406, Application US/10793626

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RESULT 8
US-10-793-626-1712
J Sequence 1712, Application US/10793626
Sequence 1712, Application US/10793626
J Publication No. US20050255478A1
J GENERAL INFORMATION:
J APPLICANT: KIMMERLY, WILLIAM JOHN
J TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS
J FILE REFERENCE: PUJ480US
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US-10-821-234-1154
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PRIOR FILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: PATENTIN VET. 2.1
SEQ ID NO 1406
LENGTH: 415
                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
7; Conserv
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Publication No. US20050255114A1
GENERAL INFORMATION:
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SEQ ID NO 1154
LENGTH: 495
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Best Local
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GENERAL INFORMATION:
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TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS
FILE REFERENCE: PU3480US
CURRENT APPLICATION NUMBER: US/10/793,626
CURRENT FILING DATE: 2004-03-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/10/821,234
CURRENT FILING DATE: 2004-04-07
PRIOR APPLICATION NUMBER: US 60/462,047
PRIOR FILING DATE: 2003-04-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Tang, Y. Tom TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
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APPLICANT: Stache-Crain, Birgit
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NAME/KEY: MOD RES
LOCATION: (415)
OTHER INFORMATION: variable amino acid
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SEQ ID NO 1712
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CURRENT FILING DATE: 2004-03-04
PRIOR APPLICATION NUMBER: 60/164,258
PRIOR FILING DATE: 1999-11-09
                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3300R1C128
CURRENT PELICATION NUMBER: US/10/131,826A
CURRENT FILING DATE: 2002-04-24
PRIOR APPLICATION NUMBER: 60/049911
PRIOR PILING DATE: 1997-06-18
PRIOR PILING DATE: 1997-08-26
PRIOR APPLICATION NUMBER: 60/059113
PRIOR PILING DATE: 1997-09-17
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APPLICANT:
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OR APPLICATION NUMBER: 60/059122
OR RILING DATE: 1997-09-17
OR APPLICATION NUMBER: 60/059184
OR APPLICATION NUMBER: 60/059263
OR APPLICATION NUMBER: 60/059263
OR RILING DATE: 1997-09-18
OR APPLICATION NUMBER: 60/059352
OR RILING DATE: 1997-09-19
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                                                                                                                                                                                                                                                                       FILING DATE: 1997-09-17
APPLICATION NUMBER: 60/059117
                                                                                                                                                                                                                                                    FILING DATE: 1997-09-
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5. US20050245730A1
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Pred. No. 44;
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           File
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Query Match
Best Local Similarity
"hes 6; Conservat
                                                                                         ; ORGANISM: Homo Sapien 
US-10-131-826A-148
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CURRENT APPLICATION NUMBER: US/10/131,826A

CURRENT FILING DATE: 2003-04-24

PRIOR APPLICATION NUMBER: 60/049911

PRIOR FILING DATE: 1997-06-18

PRIOR APPLICATION NUMBER: 60/056974

PRIOR FILING DATE: 1997-08-26

PRIOR PILING DATE: 1997-08-17

PRIOR APPLICATION NUMBER: 60/059113

PRIOR APPLICATION NUMBER: 60/059115

PRIOR FILING DATE: 1997-09-17

PRIOR FILING DATE: 1997-09-17

PRIOR APPLICATION NUMBER: 60/059117

PRIOR APPLICATION NUMBER: 60/059117

PRIOR APPLICATION NUMBER: 60/059117
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US-10-131-826A-148
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ORGANISM: Homo Sapien
US-10-131-826A-120
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NUMBER OF SEQ ID N
SEQ ID NO 148
LENGTH: 834
TYPE: PRT
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LENGTH: 775
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Best Local Similarity 55.6%;
Matches 5; Conservative
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APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                  PRIOR FILING DATE: 1997-09-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME
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APPLICATION NUMBER: 60/059117
FILING DATE: 1997-09-17
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FILING DATE: 1997-09-18
APPLICATION NUMBER: 60/059352
FILING DATE: 1997-09-19
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Wood, William
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o. US20050245730A1
                52.5%;
ilarity 54.5%;
Conservative
                                                                                                                                                                                 Application data removed - See File Wrapper or PALM NOS: 550
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                ; Score 31; DB 1; Pred. No. 71; 3; Mismatches
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Pred. No.
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US-10-131-826A-20
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US-10-131-826A-20
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Matches
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PRIOR FILING DATE: 1997-09-19
Remaining Prior Application data res
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 20
LENGTH: 867
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APPLICANT: Baker, Kevin P.
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                                                                                                                          Query Match
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1CL28
CURRENT APPLICATION NUMBER: U5/10/131,826A
CURRENT FILING DATE: 2002-04-24
PRIOR APPLICATION NUMBER: 60/049911
PRIOR FILING DATE: 1997-06-18
PRIOR FILING DATE: 1997-06-18
PRIOR APPLICATION NUMBER: 60/056974
PRIOR PRIOR APPLICATION NUMBER: 60/056974
PRIOR PILING DATE: 1997-08-26
PRIOR PILING DATE: 1997-08-26
PRIOR PILING DATE: 1997-08-26
PRIOR PILING DATE: 1997-09-17
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PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059117
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059122
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                                                                                 Local Similarity 66.
les 6; Conservative
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APPLICATION NUMBER: 60/059184
FILING DATE: 1997-09-17
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                                       4 YSRDQLLDL 12
YSKDYLTDL 195
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Wood, William
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Godowski, Paul J.
Gurney, Austin L.
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                                                                                                    52.5%;
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                                                                                 Score 31; DB Pred. No. 74; 1; Mismatches
                                                                                                                                                                                                                                                                                             See File Wrapper or
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                                                                                                                        Length 867;
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RESULT 12 US-10-793-626-1540 ; Sequence 1540, Application US/10793626

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Watches 6; Conservi
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US-10-793-626-612
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TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REFERENCE: PU3480US
CURRENT APPLICATION NUMBER: US/10/793,626
CURRENT FILING DATE: 2004-03-04
PRIOR APPLICATION NUMBER: 60/164,258
PRIOR APPLICATION NUMBER: 60/164,258
PRIOR FILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1540
LENCTH: 138
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TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REFERENCE: PU3480US
CURRENT APPLICATION NUMBER: US/10/793,626
CURRENT FILING DATE: 2004-03-04
PRIOR APPLICATION UNMBER: 60/164,258
PRIOR APPLICATION UNMBER: 60/164,258
PRIOR FILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 2328
LENGTH: 145
TYPE: DATE
Sequence 612, Application US/10793626
Publication No. US20050255478A1
GENERAL INFORMATION:
APPLICANT: KIMMERLY, WILLIAM JOHN
TITLE OF INVENTION: STRAHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REFERENCE: PU3480US
CURRENT APPLICATION NUMBER: US/10/793,626
CURRENT FILING DATE: 2004-03-04
PRIOR APPLICATION NUMBER: 60/164,258
PRIOR FILING DATE: 1999-11-09
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Local Similarity 66.7%;
hes 6; Conservative
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Pred. No. 16;
1; Mismatches
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Sequence 2192. Application US/10793626

Publication No. US20050255478A1

GENERAL INFORMATION:
APPLICANT: KIMMERLY, WILLIAM JOHN
ITITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REFERENCE: PU3480US
CURRENT APPLICATION NUMBER: US/10/793,626

CURRENT FILING DATE: 2004-03-04
PRIOR APPLICATION NUMBER: 60/164,258
PRIOR FILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2192
LENGTH: 286
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: Description of Artificial Sequence: synthetic; OTHER INFORMATION: amino acid sequence US-10-793-626-612
                                                                                                                                                                                                ; OTHER INFORMATION: Description of Artificial Sequence: synthetic; OTHER INFORMATION: amino acid sequence US-10-793-626-2192
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Search completed: November 29, Job time: 4.25 secs
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SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 612
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SUMMARIES

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ALIGNMENTS

RESULT 1 ABB96919 Human tumour antigen related peptide SEQ ID NO 14. Human; tumour; antigen; HLA-A2; cytotoxic T cell; cytostatic; cancer; 21-JUN-2002 ABB96919; ABB96919 standard; peptide; 9 AA. 31-JUL-2000; 2000JP-00231814. 30-JUL-2001; 2001WO-JP006526. 07-FEB-2002. WO200210369-A1. Homo sapiens. vaccine. Itoh K; (ITOH/) ITOH K. (first entry)

Tumor antigens inducing and/or activating HLA-A2-restricted tumor-specific cytotoxic T cells, useful in diagnosis of and screening drugs e.g. cancer vaccines for specific treatment of pancreatic cancer.

WPI; 2002-291857/33.

Claim 1; Page 21; 127pp; Japanese.

The invention relates to a peptide comprising an amino acid sequence selected from 44 fully defined amino acid sequences (ABB96906-ABB969549) and a polypeptide comprising an amino acid sequence selected from the 9 fully defined amino acid sequences (ABB969143-ABB97151). The above comprise a tumour antigen inducing or activating HLA-A2-restricted tumour specific cytotoxic T cells, which recognise HLA-A2 and a tumour antigen peptide and is thus activated. The peptides and polypeptides have cytostatic activity. The tumour antigen is useful in diagnosis of and screening drugs for specific treatment of pancreatic cancer, colon cancer and stomach cancer including in the form of vaccines. The present sequence is that of a tumour antigen peptide, useful to the invention

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specific cytotoxic T cells, useful in diagnosis of and screening drugs
e.g. cancer vaccines for specific treatment of pancreatic cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A detection method of antigen specific T-cells, comprises the use of plural antigenic peptides, useful in semi-quantitative determination of cancer specific T-cell frequencies and for monitoring cellular immunity.
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                                                        Binding peptide; cell death; cell
                                                                                                     A human eukaryotic Initiation Factor 4E
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                            Homo sapiens
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9; Conserva
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                                                                                                                                    (first entry)
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 Location/Qualifiers
                                                         apoptosis;
                                                                       eukaryotic Initiation Factor 4G; eIF4G;
                                                                                                                                                                                                                                                                                                                                                100.0%;
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                                                           anticancer;
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Pred. No.
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2e+06;
                                                           antitumor
                                                                                                     (eIF4E) binding peptide.
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RESULT 5
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Best Local
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cell death; cell
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9; Conser
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/label= Lys,
                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                        /note= "unspecified residue specification"
                                                                                                                                                                                                                                                                                                                                                                                                                    eukaryotic
apoptosis;
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anticancer; antitumor.
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          The present sequence represents a binding peptide for an eukaryotic Initiation Factor 45 (eIF45) protein. The specification describes eland eIF45 binding agents, such as peptides or peptidemimetics. These binding agents are used for the induction of cell death. The binding peptides are used for inducing cell apoptosis. They are used in pharmaceutical compositions for anticancer or antitumor treatment of mammalian cells. Specifically, the peptides result in growth inhibit
                                                                                                                                                  Use of eukaryotic Initiation Factor 4E (elF4E) binding agents e.g. elF4E-binding peptide (elF4E-BP) derivatives as anticancer or antitumor agents for inducing apoptosis in e.g. mammalian tumor cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Binding peptide;
cell death; cell
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 or increased cytotoxicity to tumour
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9; Conserv
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apoptosis;
                                                                                                                           46pp; English.
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100.0%;
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anticancer; antitumor.
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0.024;
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describes eIF4G
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Best Local S
Matches 9
                               Matches
                                               Query Match
Best Local :
                                                                                                                    a 4E-BPI (a member of eukaryotic initiation factor 4E (eIF-4E)-binding protein 1) shows a phenotype of an altered glucose and/or fat metabolism when compared to a control animal. The products of the invention have antidiabetic and ancrectic activity. The non-human transgenic animals are useful as models for the investigation of lipid and glucose metabolism, energy homeostasis and associated diseases. The transgenic animals are also useful for selection and identification of modulators of the expression and/or activity of 4E-BPI and for screening drugs to isolate therapeutic agents which are useful as anti-obesity, anti-fat deposition disorder, anti-diabetes and anti-metabolic diseases associated with fat deposition disorders. The effect of the disruption of 4E-BPI an modulate fat tissue growth, glucose metabolism and weight gain in an animal
                                                                                                                                                                                                                                                                                                                                                                                                                  Non-human transgenic animal useful as model for studying lipid and glucose metabolism, has germ and somatic cells containing knockout mutation in DNA encoding eukaryotic initiation factor 4E-binding protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryotic initiation factor; eIF4E; transgenic animal; antidiabetic; knockout mutation; 4E-BP1; glucose metabolism; fat metabolism; anorectic; drug; anti-obesity; anti-fat deposition; anti-metabolic.
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                                                                                            Sequence 16 AA;
                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Fig 7; 80pp; English
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02-FEB-2000; 2000US-0179743P.
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                               Similarity 9; Conserv
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                                 Conservative
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                                              97.9%;
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100.0%; Pred. No.
tive 0; Mismatc
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Pred. No.
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                                 Mismatches
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0.032;
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                                                                                            RESULT 9
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Best Local :
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                                 AAB11095 standard;
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02-FEB-2000; 2000US-0179743P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            glucose metabolism and weight gain
                             peptide;
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02-FEB-2000; 2000US-0179743P
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                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 16
Eukaryotic initiation factor; eIF4E; transgenic animal; antidiabetic; knockout mutation; 4E-BP1; glucose metabolism; fat metabolism; anorectic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Fig 7; 80pp; English
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                                                      Chicken eIF-4E recognition motif peptide 4E-BP
                                                                                            16-FEB-2001
                                                                                                                                                                    AAB11099 standard; peptide; 16
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                                                                                                                                                                                                                                                                                                                                     97.9%; Score 46; DB 3; Length 16; 100.0%; Pred. No. 0.032; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              drug; anti-obesity; anti-fat deposition; anti-metabolic.
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                                                                                                               Eukaryotic initiation factor; eIF4E; transgenic animal; antidiabetic; knockout mutation; 4B-BP1; glucose metabolism; fat metabolism; anorec drug; anti-obesity; anti-fat deposition; anti-metabolic.
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                                                                                                                                                                                 eIF-4E recognition motif peptide h4E-BP1
                                                                                                                                                                                                                                                 AAB11085;
                                                                                                                                                                                                                                                                                  AAB11085 standard; peptide; 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tissue growth, glucose metabolism and weight gain in an
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2000US-0179743P
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                                                                                                                                                                                                                    entry)
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                                                                                                                                                                                                                               Eukaryotic initiation factor; eIF4E; transgenic animal; antidiabetic; knockout mutation; 4E-BP1; glucose metabolism; fat metabolism; anorec drug; anti-obesity; anti-fat deposition; anti-metabolic.
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02-FEB-2000;
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02-FEB-2000; 2000US-0179743P.
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Sonenberg N,
                                                                                                        07-APR-2000; 2000WO-CA000388.
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Tremblay M,
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Tsukiayama-Kohara
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                            Non-human transgenic animal useful as model for studying lipid and glucose metabolism, has germ and somatic cells containing knockout mutation in DNA encoding eukaryotic initiation factor 4E-binding p
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02-FEB-2000; 2000US-0179743P
                                                                                                                                                                                                                                                                                                                                                                   Eukaryotic initiation factor; eIF4E; transgenic animal; antidiabetic; knockout mutation; 4E-BP1; glucose metabolism; fat metabolism; anorec drug; anti-obesity; anti-fat deposition; anti-metabolic.
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                                                                                              WPI; 2000-672657/65
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(a member of eukaryotic initiation factor 4E (eIF-4E)-binding
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Disclosure;

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80pp;

English

cells and invention

somatic cells contain a knockout

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                                                                   This invention describes a novel non-human transgenic animal (I) whose germ cells and somatic cells contain a knockout mutation in DNA encodis a 4E-BP1 (a member of eukaryotic initiation factor 4E (eIF-4E)-binding
                                                                                                                                                                                                                                            Non-human transgenic animal useful as model for studying lipid and glucose metabolism, has germ and somatic cells containing knockout mutation in DNA encoding eukaryotic initiation factor 4E-binding p
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protein 1) shows a phenotype of an altered glucose when compared to a control animal. The products of antidiabetic and anorectic activity. The non-human
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0.032;
     kout mutation in DNA encoding factor 4E (eIF-4E)-binding factors and/or fat metabolism ucts of the invention have n-human transgenic animals are
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01-DEC-2000; 2000WO-CA001465

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99US-0168398P.

(WINC-) UNIV MCGILL

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Sonenberg

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Polunavsky VA,

Bitterman

07-JUN-2001.

AABB4401-15 represent 4B-binding sites. 4E-binding protein 1 (4E-BP1) is a repressor of cap-dependent translation initiation, and selectively activates apoptosis in Ras-transformed fibroblasts and eliminates Ras-induced chemoresistance. The effects of 4E-BP1 are strictly dependent on its ability to sequester the translation initiation factor elP4E, thereby preventing its assembly into an active pre-initiation complex. The specification describes a method for inducing apoptosis in a cell in which the apoptosis pathway is inhibited. The method comprises decreasing the amount of elF4F pre-initiation complex by sequestration of elF4E, thus relieving an apoptosis block. The method is useful for modulating pro-apoptotic and anti-apoptotic pathways in cells, especially in Ras-transformed cells. Thus, the method is useful for treating cancer. The elF4E sequestering agent, 4E-BP1 or its elF4E binding portion is useful for treating high proliferative cells

Inducing apoptosis in a cell in which the apoptosis pathway is inhibited, useful for treating cancer or highly proliferative cells, comprises decreasing the amount of elF4F pre-initiation complex, relieving an

Disclosure; Fig 6; 80pp; English

apoptosis block

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RESULT 15
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                                                                                                                                                                                                                                                                                                                                                                                                              4E-binding site; 4E-binding protein; 4E-BP; 4E-BP1; chemoresistance; cap-dependent translation initiation repressor; apoptosis; translation initiation factor; elF4E; Ras; cancer.
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Qy 1 RIIYDRKFL 9
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   pred, No. is the number of results predicted by chance to have a
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Copyright (c) 1993 - 2005 Compugen Ltd.
 A57396
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RESULT 2 A55258 insulin-stimulated phosphoprotein PHAS-I - rat C;Species: Rattus norvegicus (Norway rat) C;Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 09-Jul-200 C;Accession: A55258; A54719 R;Hu, C; Pang, S; Kong, X.; Velleca, M.; Lawrence Jr., J.C. Proc. Natl. Acad. Sci. U.S.A. 91, 3730-3734, 1994 A;Title: Molecular cloning and tissue distribution of PHAS-I, an intracell A;Reference number: A55258; MUID:94224815; PMID:8170978 A;Accession: A55258 A;Molecule type: mRNA A;Residues: 1-117 <hun- #status="" \$8-69="" \$90-69="" (by="" (covalent)="" (map)="" (ser)="" 58-69="" <hay's="" a;cross-references:="" a;residues:="" a;title:="" binding="" by="" c;keywords:="" expe<="" f;64="" gb:u05014;="" kina="" kinase)="" map="" mitogen-activated="" nid:="" of="" phas-i="" phosphate="" phosphoprotein="" phosphorylation="" protein="" shosphoprotein="" site:="" td="" uniparc:upi00000e729c;="" uniprot:q62621;="" uniprot:q62622;=""><td>RESULT 1 A57396 PHAS-I protein - mouse C;Species: Mus musculus (house mouse) C;Date: 23-Feb-1996 #sequence_revision 23-Feb-1996 #text_change 09-Jul-200 C;Accession: A57396 R;Lin, T.A.; Kong, X.; Saltiel, A.R.; Blackshear, P.J.; Lawrence Jr., J.C. J. Blol. Chem. 270, 18531-18538, 1995 A;Title: Control of PHAS-I by insulin in 3T3-L1 adipocytes. Synthesis, deg A;Title: Control of PHAS-I by insulin in 3T3-L1 adipocytes. Synthesis, deg A;Title: Control of PHAS-I by insulin in 3T3-L1 adipocytes. Synthesis, deg A;Title: Control of PHAS-I by insulin in 3T3-L1 adipocytes. Synthesis, deg A;Title: Control of PHAS-I by insulin in 3T3-L1 adipocytes. Synthesis, deg A;Title: Control of PHAS-I by insulin in 3T3-L1 adipocytes. Synthesis, deg A;Title: Control of PHAS-I by insulin in 3T3-L1 adipocytes. Synthesis, deg A;Title: Control of PHAS-I by insulin in 3T3-L1 adipocytes. Synthesis, deg A;Title: Control of PHAS-I by insulin in 3T3-L1 adipocytes. Synthesis, deg A;Title: Control of PHAS-I by insulin in 3T3-L1 adipocytes. Synthesis, deg A;Title: Control of PHAS-I by insulin in 3T3-L1 adipocytes. Synthesis, deg A;Title: Control of PHAS-I by insulin in 3T3-L1 adipocytes. Synthesis, deg A;Title: Control of PHAS-I by insulin in 3T3-L1 adipocytes. 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Synthesis of Control of PHAS-I by insulin insulin i</td><td>30 32 68.1 388 2 D72200 ornithine decarbox 31 32 68.1 454 2 PC4237 trans-cinnamate 4- 32 68.1 454 2 T37933 32 32 68.1 454 2 T37933 33 68.1 503 2 H81366 trans-cinnamate 4- 34 32 68.1 505 2 JC5129 35 32 68.1 505 2 JC5129 36 68.1 505 2 S68204 trans-cinnamate 4- 37 32 68.1 505 2 S68204 trans-cinnamate 4- 38 32 68.1 505 2 A47454 trans-cinnamate 4- 39 32 68.1 505 2 T09525 trans-cinnamate 4- 40 32 68.1 505 2 T09525 trans-cinnamate 4- 41 32 68.1 506 2 T0458 crytochrome P450 - 42 32 68.1 506 2 T14907 43 32 68.1 705 2 T34477 44 32 68.1 859 2 G86242 hypothetical prote 45 31.5 67.0 601 2 T26062</td></hun->	RESULT 1 A57396 PHAS-I protein - mouse C;Species: Mus musculus (house mouse) C;Date: 23-Feb-1996 #sequence_revision 23-Feb-1996 #text_change 09-Jul-200 C;Accession: A57396 R;Lin, T.A.; Kong, X.; Saltiel, A.R.; Blackshear, P.J.; Lawrence Jr., J.C. J. Blol. Chem. 270, 18531-18538, 1995 A;Title: Control of PHAS-I by insulin in 3T3-L1 adipocytes. Synthesis, deg A;Title: Control of PHAS-I by insulin in 3T3-L1 adipocytes. Synthesis, deg A;Title: Control of PHAS-I by insulin in 3T3-L1 adipocytes. Synthesis, deg A;Title: Control of PHAS-I by insulin in 3T3-L1 adipocytes. Synthesis, deg A;Title: Control of PHAS-I by insulin in 3T3-L1 adipocytes. Synthesis, deg A;Title: Control of PHAS-I by insulin in 3T3-L1 adipocytes. Synthesis, deg A;Title: Control of PHAS-I by insulin in 3T3-L1 adipocytes. Synthesis, deg A;Title: Control of PHAS-I by insulin in 3T3-L1 adipocytes. Synthesis, deg A;Title: Control of PHAS-I by insulin in 3T3-L1 adipocytes. Synthesis, deg A;Title: Control of PHAS-I by insulin in 3T3-L1 adipocytes. Synthesis, deg A;Title: Control of PHAS-I by insulin in 3T3-L1 adipocytes. Synthesis, deg A;Title: Control of PHAS-I by insulin in 3T3-L1 adipocytes. Synthesis, deg A;Title: Control of PHAS-I by insulin in 3T3-L1 adipocytes. Synthesis, deg A;Title: Control of PHAS-I by insulin in 3T3-L1 adipocytes. Synthesis, deg A;Title: Control of PHAS-I by insulin in 3T3-L1 adipocytes. Synthesis, deg A;Title: Control of PHAS-I by insulin in 3T3-L1 adipocytes. Synthesis, deg A;Title: Control of PHAS-I by insulin in 3T3-L1 adipocytes. Synthesis, deg A;Title: Control of PHAS-I by insulin in 3T3-L1 adipocytes. Synthesis, deg A;Title: Control of PHAS-I by insulin in 3T3-L1 adipocytes. Synthesis, deg A;Title: Control of PHAS-I by insulin in 3T3-L1 adipocytes. Synthesis, deg A;Title: Control of PHAS-I by insulin in 3T3-L1 adipocytes. Synthesis, deg A;Title: Control of PHAS-I by insulin in 3T3-L1 adipocytes. Synthesis, deg A;Title: Control of PHAS-I by insulin in 3T3-L1 adipocytes. 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Query Match Best Local Similarity

97.9%;

Score 46; pred. No.

DB 2; 0.038;

Length 117;

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R;Pause, A.; Belsham, G.J.; Gingras, A.C.;
Nature 371, 762-767, 1994
                                                                                                                                                                                                                                                                                                                                                      4E-BP2 protein - human
C;Species: Homo sapiens (man)
C;Date: 28-Oct-1996 #sequence_revision 27-Feb-1997 #text_change 09-Jul-2004
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A;Residues: 1-118 <NIS>
A;Residues: 1-118 <NIS>
A;Cross-references: UNIPARC:UPI00006E50A
A;Cross-references: UNIPARC:UPI00006E50A
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C;Date: 14-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004
C;Accession: S50866; JCS899
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A; Residues: 1-120 < PAU>
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A;Title: Expression of a synthetic gene for initiation factor A;Reference number: JC5899; MUID:98162949; PMID:9504423
A;Accession: JC5899
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Nature 371, 762-767, 1994
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A;Residues: 1-118 <PAU>
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A;Kiatus: preliminary
A;Molecule type: mRNA
A;Residues: 1-1680 <ROE>
A;Residues: 1-1680 <ROE>
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C;Accession: A43434
R;Roebroek, A.J.; Creemers, J.W.; Pauli, I.G.; Kurzik-Dumke, U.; Rentrop, M.; Gatetr
J. Biol. Chem. 267, 17208-17215, 1992
A;Title: Cloning and functional expression of Dfurinz, a subtilisin-like proprotein
A:Reference number: A43434; MUID:92381036; PMID:1512259
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Best Local Similarity
Watches 6; Conserve
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C;Superfamily: phage T4 DNA-directed DNA polymerase
C;Keywords: DNA binding; DNA replication; nucleotidyltransferase
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Eur. J. Biochem. 172, 553-563, 1988
A;Title: Deoxycytidylate hydroxymethylase gene of bacteriophage T4: nucleotide sequence charactering number: JF0071; MUID:88166734; PMID:3350013
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A;Title: Primary structure of T4 DNA polymerase.
A;Reference number: A28165; MUID:88227938; PMID:3286635
A;Accession: A28165
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C;Date: 17-Mar-1987 #sequence revision 30-Jun-1987 #text_change 09-Jul-2004
C;Accession: JS0791; PU0006; A28165; JU0097; A00717
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A;Cross-references: UNIPARC:UPI000016D7A7; GB:M37159; GB:M28192; NID:g215839; PIDN:AAA21;
C;Comment: This enzyme is required for both initiation and maintenance of viral DNA repli
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A;Cross-references: FlyBase:FBgn0004598
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A; Residues: 1-898 <SP3>
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A;Accession: PU0006
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A; Residues: 1-898 <SPI>
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                                                                                                                                                                                                                                                                                                                                                Rentrop, M.; Gateff, E.
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C;Keywords: hydrolase; serine proteinase; transmembrane protein F;409-652/Domain: subtilisin homology <SBT> F;418,457,638/Active site: Asp, His, Ser #status predicted
                                                                                                                                                                                                                                                                R;Petri, J.B.; Schmieger, H. Gene 88, 47-55, 1990
A;Title: Isolation of fragments with pac function for phage A;Reference number: PQ0093; MUID:90255967; PMID:2341038
A;Accession: JQ0531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene 3 protein - phage LP-7 C;Species: nhace in 7
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A; Residues: 1-162 <PET>
A; Cross-references: UNIPARC: UPI0000136BE0;
C; Comment: This protein is involved in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: phage LP-7
C;Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change
C;Accession: JQ0531
RESULT 9
B96966
beta-mannanase ManB-like enzyme, contains ChW-repeats [imported] -
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A; Residues: 1-291 < STO>
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Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                               :Cross-references: UNIPROT:Q9M140; UNIPARC:UPI00000A6604; GB:NC_001268; NID:g7267627;
                                                                                                                                                                                                                                                      Statue: preliminary
                                                                                                                                                                                      Gene: AT4g01300
                                                                                                                                                                          position: 4
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75.0%;
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Pred. No.
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Pred. No.
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Pred. No. 28;
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                                                                                                                                               Length 291
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C;Species: Clostridium acetobutylicum
C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
C;Accession: B96966
R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacter A;Beference number: A96900; MUID:21359325; PMID:21359325
A;Accession: B96966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Scheet, P.; Magg1, L. submitted to the EMBL Data Library, June 1997 submitted to the EMBL Data Library, June 1997 A;Description: The sequence of A. thaliana IG002N01. A:Reference number: Z14407
C;Accession: B86194
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso; Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K., ansen, N.F.; Hughes, B.; Hulzar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Accession: B86194
A;Accession: B86194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Residues: 1-531 <KUR>
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                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
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A; Introns: 78/2; 169/1; 234/3; 301/3; 387/3; 528/1; 974/1
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A; Residues: 1-1028 < SCH>
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77.8%;
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71.4%;
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Pred. No.
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Pred. No. 1e+02;
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52;
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R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Fgasawarra, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. DNA Res. 8, 11-22, 2001
A;Ritle: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: D90955
                                                                                                                                                                                                                                                                                                                                C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004 C;Accession: A85804  
C;Accession: A85804  
R;Perna, N. T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, Iller, L.; Grotbeck, B.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, Nature 409, S29-S33, 2001  
A;Tille: Genome sequence of enterohemorrhagic Escherichia coli O157:H7. A;Reference number: A85480; MUID:21074935; PMID:11206551
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A;Residues: 1-1251 <STO>
A;Cross-references: UNIPROT:Q9MA34; UNIPARC:UPI00000A4622; GB:AE005172; NID:g6850321;
  밁
                                                                                                                                                                                                    A;Molecule type: DNA
A;Residues: 1-107 <870>
A;Residues: 1-107 <870>
A;Cross-references: UNIPROT:Q8XCD6; UNIPARC:UPI0000D04B0; GB:AE005174; NID:g12515970;
A;Experimental source: strain O157:H7, substrain EDL933
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A;Residues: 1-107 <HAY>
A;Cross-references: UNIPROT:QBXCD6; UNIPARC:UPI00000D04B0; GB:BA000007; PIDN:BAB36035.1.
A;Experimental source: strain O157:H7, substrain RIMD 0509952
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein Z2959 [imported] - Escherichia coli (strain O157:H7, substrain
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/Species: Escherichia coli
/pate: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
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Best Local
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 Mismatches

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Pred. No. 16;
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3; Mismatches 0;
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C;Accession: F69873
C; Bron, S; Brouillet, S; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cho', Fernst, S; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cho', A; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E. Nature 390, 249-256, 1997
A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler, Inch., J.; Kochingstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, Goetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, J.; Mathors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel, Y.; M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetellé, R.; Gayawa, K.; Ogiwara, A.; Cocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Sanlon, A.; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Serot, akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama, T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K. A; Mathors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis. A, Reference number: A69580; MUID:98044033; PMID:9384377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: UNIPROT:P76308;
A;Experimental source: strain K-12,
C;Superfamily: Escherichia coli hypo
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A;Title: The complete genome sequence of Escherichia coli K-12. A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Accession: H64953
                                                                                                                                                                                                                                                                                                                       A;Cross-references: UNIPROT:034743; A;Experimental source: strain 168
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A; Residues: 1-107 <BLAT>
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C;Species: Bacillus subtilis
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
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	2; Len 15; 0;	nic_DNA. 1C30996 CRC64;	derived from un (WGS) ent		Tetraodon nigrovi	Saurin W., Scarpell J., Roest Crollius	J., McJ	a M., Vac	Doss	L., Sta		eleostei; ; Tetraod	7	enbas	e update)	3 AA.	и́						
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10-OCT-2003 (Rel. 42, Createu, 10-OCT-2003 (Rel. 42, Last sequence update) 13-SEP-2005 (Rel. 48, Last annotation update) Eukaryotic translation initiation factor 4E-binding (ATF4E-binding protein 3).
                                                   HGNC; HGNC:3290;
MIM; 603483; -.
                                                                                                                                                            This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                   use
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MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
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LEU-45, AND TISSUE SPECIFICITY
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        InterPro;
       GO:0016281; C:eukaryotic translation initiation GO:0030371; F:translation repressor activity; NA GO:0045947; F:negative regulation of translation erPro; IPR008606; EIF4EBP.
                                                                                                                                                                                                                                                                                        mouse cDNA sequences.";
c. Natl. Acad. Sci. U.S.A.
                                                                                                                                                   as
                                                                                                                                                                                                                          c. Natl. Acad. Sci. U.S.A. 99:16899-16903(20 FUNCTION: Regulates eIF4E activity by preve the eIF4F complex. SUBUNIT: EIF4EBP3 interacts with EIF4E. TISSUE SPECIFICITY: Expression is highest i heart, kidney, and pancreas, whereas there expression in brain and thymus.
                                                                                                                                                                                                   PTM: Phosphorylated.
SIMILARITY: Belongs to the eIF4E-binding
                                                                      AF038869; AAC39761.1; -; n

,; BC010881; AAH10881.1; -; n

,; BC063293; AAH69293.1; -; n

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Eutheria;
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A Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
A Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
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Wincker P., Lander E.S., Weissenbach J., Roest Crollius H.,
"Genome duplication in the teleost fish Tetraodon nigroviridis reveals
the early vertebrate proto-karyotype.";
                                                                                                    Matches
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                                                                                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE.
Genoscope; whitehead Institute Centre for Genome Research;
Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry whi
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SEQUENCE
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Eukaryota; Metazoa; Chordata; Craniata; Ve.
Actinopterygii; Neopterygii; Teleostei; Eu
Acanthomorpha; Acanthopterygii; Percomorph
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Phosphorylation;
MUTAGEN 40
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horylation; Protein synthesis
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1 SCAF14998, whole genome shotgun sequence.
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A Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

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A Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

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Bosek S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

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Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schemtz J., Myers R.M.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

"Generation and initial analysis of more than 15,000 full-length human

"Generation and initial analysis of more than 15,000 full-length human
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
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Eukaryotic translation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                                                            InterPro; IPR008606; EIF4EBP.
PANTHER; PTHR12669; EIF4EBP; 1.
Phosphorylation; Protein synthe
                                                                                                                                                                                                                                                                                                                                                                            EMBL; AY226182; AAO73448.1; -; mRNA.
EMBL; BC061242; AAH61242.1; -; mRNA.
Ensembl; ENSMUSG0000003775; Mus musculus
MGI; MGI:1270847; E1f4ebp3.
                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mouse cDNA sequences.";

c. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

rUNCTION: Regulates cif4Es activity by preventing its assembly into the elf4F complex (By similarity).

SUBUNIT: EIF4EBB3 interacts with EIF4E (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PTM: Phosphorylated (By similarity). SIMILARITY: Belongs to the eIF4E-binding protein family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Swiss-Prot entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation European Bioinformatics Institute. There are no restrictions on it
37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EuoT
                                                                                                                       Similarity
9; Conserv
                                                              RIIYDRKFL 9
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                                                                                                                                                                                                                                                    101
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                                                                                                                          Conservative
                                                                                                                                                                                                                                                    8
                                                                                                                                                                                                                                                 Protein synthesis inhibitor; Ti
1; 11019 MW; 78F82052696A9BD7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
n initiation factor 4E-binding protein 3 (4E-BP3)
n 3).
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                                                                                                                                                        Score 46; DB 1;
Pred. No. 0.17;
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RESULT 5 Q9BG57_PIG

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RESULT 6
QSUJD2 BRARE
QSUJD2 BRARE PRELIMINARY;
AC
QSUJD2;
DT 01-FEB-2005 (TrEMBLrel. 29,
DE 2005 (Captains)
CR Actinopterygii, Neopterygii;
OC Actinopterygii, Neopterygii,
OC Actinopterygii, Neopterygii, Neopterygii,
OC Actinopterygii, Neopterygii, Neopterygii,
OC Actinopterygii, Neopterygii, N
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                          RX MEDLINE=2238857; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Stapleton M., Gares M.B., Bonaldo M.F., Carainci P., Prange C.,
RA Brownstein M.J., Usdin T.B., Bonaldo M.F., Carainci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Pahey J., Helton E., Ketteman M., Madan A., Gay L.J., Hulyk S.W.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J.M., Warra M.A.;
"Generation and initial analysis of more than 15,000 full-length human defence CDNA sequences.";
"Tand mouse cDNA sequences.";
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Best Local S
Matches 9
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01-JUN-2001
01-MAR-2004
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NON TER
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9BG57_PIG
Q9BG57;
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Mammalia; Butheria; Laurasiatheria; Cetartiodactyla;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF05456; eIF_4EBP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sus scrofa (Pig).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Brachydanio rerio (Zebrafish)
Bukaryota; Metazoa; Chordata;
Actinopterygii; Neopterygii; T
Cyprimidae; Danio.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 41
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9; Conserv
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102 AA;
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5 (TrEMBLrel. 29,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97.9%;
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Last annotation updat
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; Craniata; Vertebrata; Euteleostomi;
Teleostei; Ostariophysi; Cypriniformes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 46; DB 2;
Pred. No. 0.17;
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                 99:16899-16903 (2002)
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Matches
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Q98TT6;
10-MAY-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (NOV-2004) to the EMBL/GenBank/DDBJ databases.

BMBL; BCO85595; AAH85595.1; -; mRNA.

ZFIN; ZDB-GENE-041114-44; zgc;103720.

GO; GO:0008190; F:eukaryotic initiation factor 4E binding; IEA.

GO; GO:0045947; P:negative regulation of translational initia.

InterPro; IPRO08606; EIF4EBP.

Pfam; PP05456; eIF 4EBP; 1.

SEQUENCE 104 AA; 11427 MW; 446DF0D99AEFB750 CRC64;
                                                                                                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].

NIH - Zebrafish Gene Collection (ZGC) project;

Submitted (JAN-2003) to the EMEL/GenBank/DDBJ databases.
-!- FUNCTION: Regulates eif4ela activity by preventing its and into the eIF4F complex (By similarity).
-!- SUBUNIT: Interacts with eif4ela.
-!- SIMILARITY: Belongs to the eIF4E-binding protein family.
                                                        ZFIN; ZDB-GENE-030131-3211; Zgc:56330.
GO; GO:0005515; F:protein binding; IDA.
GO; GO:0030371; F:translation repressor activity; ISS.
GO; GO:0045947; P:negative regulation of translational initia.
InterPro; IPR008606; EIF4EBP.
                                                                                                                                EMBL; AF332983; AAG50053.1; -; mRNA.
EMBL; BC046079; AAH46079.1; -; mRNA.
Ensembl; ENSDARG00000023315; Danio r
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10-MAY-2005 (Rel. 47, Created)
10-MAY-2005 (Rel. 47, Last senence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Eukaryotic translation initiation factor 4E-lA-binding
Enkaryotic translation (4E-BP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BRARE
                                                                                                                                                                                                                                                                                                                                                                                                                     NUCLEOTIDE SEQUENCE [MRNA], AND INTERACTION PubMed=14701818, DOI-10.1074/jbc.M313688200; Robalino J., Joshi B., Fahrenkrug S.C., Jagu "Two zebrafish eIF4E family members are diff functionally divergent.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Brachydanio rerio (Zebrafish)
Eukaryota; Metazoa; Chordata;
Actinopterygii; Neopterygii; T
Cyprinidae; Danio
 SEQUENCE
                             PANTHER; PTHR12669; EIF4EBP; 1.
Pfam; PF05456; eIF_4EBP; 1.
                                                                                                                                                                                                              иве
                                                                                                                                                                                                                            the
                                                                                                                                                                                                                                                          This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORFNames=zgc:56330;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Director MGC Project;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                            Biol.
                                                                                                                                                                                                              96
                                                                                                                                                                                                                            European
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9; Conserv
synthesis Inhibitor; Translation regulation
112 AA; 12531 MW; F71BEA295722826E CRC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                           rot entry is copyright. It is produced through a collaboration Swiss Institute of Bioinformatics and the EMBL outstation - Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                             ioinformatics Institute. There are no restrictions its content is in no way modified and this statement
                                                                                                                                                                                                                                                                                                                                                                                                            279:10532-10541(2004).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ) (Danio rerio).
; Craniata; Vertebrata; El
Teleostei; Ostariophysi;
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0.17;
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differentially expressed
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 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EIF4E1A
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i; Cypriniformes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein
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Query Match

97.98;

Score

46;

DB 1;

Length 112;

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RA Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,

RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,

RA Micaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,

RA Anthouard V., Jubin C., Castelli V., Boudet N., Castellano S.,

RA Anthouard V., Jubin C., Castelli V., Butlika M., Vacherie B.,

RA Anthouard V., Jubin C., Catellio L., Poulain J., De Berardinis V.,

RA Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,

RA Cruaud C., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,

RA Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,

RA Kellis M., Volff JN., Guigo R., Zody M.C., Mesirov J.,

RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,

RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,

RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,

RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,

RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,

RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,

RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,

RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,

RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,

RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,

RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,

RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,

RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,

RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,

RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,

RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,

RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,

RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,

RA L
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Best Local S
Matches 9
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                                                                                                       Q6DJI1;
25-OCT-2004 (TrEMB:
25-OCT-2004 (TrEMB:
25-OCT-2004 (TrEMB:
MGC83416 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; CAA
NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tetraodon nigroviridis (Green puffer).
Eukaryota; Metazoa; Chordata; Craniata; Verte
Actinopterygii; Neopterygii; Teleostei; Eutel
Acanthomorpha; Acanthopterygii; Percomorpha;
Tetraodontoidea; Tetraodontidae; Tetraodon.
Eukaryota; Metazoa;
Amphibia; Batrachia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genoscope; Whitehead Institute Centre for Genome Research; Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13-SEP-2005 (TrEMBLrel. 31, Created)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Chromosome 17 SCAF14563, whole genome shotgun sequen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q4SL38 TETNG
Q4SL38;
                                                                                      Name=MGC83416;
                                                                                                                                                                                                                                                      Q6DJI1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=99883;
                                                   Xenopus laevis (African
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUCLEOTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORFNames=GSTENG00016435001;
                                                                                                                                                                                                                                                                                YENLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TETNG
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preliminary data.
preliminary data.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL/GenBank/DDBJ whole
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CAAE01014563;
TER 112 1
NCE 112 AA;
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9; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                             (TrEMBLrel.
                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
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  ican clawed frog).
Chordata; Craniata; Ve;
; Anura; Mesobatrachia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; +1
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Last anno
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Pred. No
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; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A158734EE80064E1 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      here is derived
                                                                                                                                         sequence up
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    No.
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0.18;
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Euteleostei; Neoteleostei;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0.18;
                               Vertebrata;
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     Pipoidea;
                                                                                                                                      update)
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                               Euteleostomi;
     Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      an
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RESULT 10
Q6NUG4 XENLA
ID Q6NUG47
AC Q6NUG47
DT 05-JUL-2
DT 05-JUL-2
DT 05-JUL-2
DT 05-JUL-2
DT MGC789B9
GN Names-MGC
OS Xenopus
OC Eukaryoto
OC Amphibie
OC Xenopodi
OX NCBI_Tax
RN [1]
RP NUCLEOTI
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RRA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RRA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RRA Altechul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RRA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RRA Diatchenko L., Marusina K., Farmer Y.A., Rubin G.M., Hong L.,
RRA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RRA Browmstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RRA Browmstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RRA Browmstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RRA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RRA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RRA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RRA Willialon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RRA Rahesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RRA Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M.,
RRA Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M.,
"Generation and initial analysis of more than 15,000 full-length human
"Generation and initial analysis of more than 15,000 full-length human
"Generation and initial analysis of more than 15,000 full-length human
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Best Local S
Matches
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05-JUL-2004 (TrEMBLrel.
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MGC78987 protein
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Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC075198; AAH75198.1; -; mRNA,
GO; GO:0008190; F:eukaryotic initiation factor 4E binding; IEA.
GO; GO:0045947; P:negative regulation of translational initia.
InterPro; IPR008606; EIF4EBP.
Pfam; PF05456; eIF 4EBP; 1.
SEQUENCE 113 AA; 12459 MW; DAAB4CF04367F1CC CRC64;
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NCBI_TaxID=8355;
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                                                                                                                  Xenopus laevis (African clawed frog).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopudinae; Xenopus; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                Q6NUG4 XENLA PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=22341132; PubMed=12454917; [
Klein S.L., Strausberg R.L., Wagner
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                                                                                                                                                                                                                                              Name=MGC78987;
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         TISSUE-Embryo
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Q6NYL2 DT 05-JUL-2
RA NACHOOPTING
OC Cyprinid
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OC NCBI Tax
RN [1]
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RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Stapleton M.J., Osares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Stapleton M.J., Usdin T.B., Toshiyuki S., Carrinci P., Prange C.,
RA Stapleton M.J., Usdin T.B., Toshiyuki S., Carrinci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Raha S.S., Mozley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Generation and initial analysis of more than 15,000 full-length human
Terminal Envise C.N.M. Generation and initial analysis of more than 15,000 full-length human
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Best Local S
Matches 9
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Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC068624; AAH68624.1; mRNA.
GO; GO:0008190; F:eukaryotic initiation factor 4E binding; IEA
GO; GO:0008190; P:eukaryotic regulation of translational initia.
GO; GO:0045947; P:negative regulation of translational initia.
InterPro; IPR008606; EIF4EBP.
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  MEDLINE-2238257; PubMed-12477932; DOI=10.1073/pnas.242603899; Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata
Actinopterygii; Neopterygii;
Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                  05-JUL-2004 (TrEMBLrel. 27, Last sequence update) 05-JUL-2004 (TrEMBLrel. 27, Last annotation update) Eukaryotic translation initiation factor 4E binding
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Q6NYL2;
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                                                                                                                        TISSUE=Kidney;
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                                                                                                                                                                                                                                                                                                               Name=eif4ebp2;
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c. Natl. Acad. Sci. U.S
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NCE 113 AA; 12430 MW;
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Metazoa; Chordata;
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sberg R.L., Wagner L., Pontius J., Clifton S.W.,
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Teleostei; Osta
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RA KLausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., RA Altschul S.F., Zeeberg B., Button, K., Schaefer C.F., Bhat N.K., RA Altschul S.F., Zeeberg B., Button, Max S.I., Wang J., Hsieh F., RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., RA Hopkins R.F., Jordan H., Moore T., Rubin G.M., Hong L., Scheetz T.E., Stateleton M.J., Usdin T.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., A Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Vallalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Vallalon D.K., Walen A., Young A.C., Shevchenko Y., Bouffard G.G., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Va Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Va Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
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Stepleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Raha S.S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Rodriguez A.C., Grimwood J., Schmutz J., Wyers R.M.,
Rodriguez A.C., Grimwood J., Schmutz J., Wyers R.M.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.',
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
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GO; GO:0008190; F:eukaryotic initiation factor 4E binding; GO; GO:0003743; F:translation initiation factor activity; I GO; GO:0045947; P:negative regulation of translational init InterPro; IPRO88606; EIF4EBP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=22388257;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Amphibia; Batrachia; Anura;
Xenopodinae; Xenopus; Silura
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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(TrEMBLrel. 27, Last sequence update)
(TrEMBLrel. 27, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97.9%; Pred. No.
100.0%; Pred. No.
17e 0; Mismatches
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                                                  MEDLINE-22354683; PubMed=12466851; DOI=10.1038/nature01266;

AD Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,

AN ANIkaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,

AN ANIkaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,

AN ANIkaido I., Osato N., Saito R., Schonbach C., Gojobori T.,

AN ANIKAIDI R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,

AN Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,

AN Baldarelli R., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,

AN Balake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,

AN Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,

AN Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,

AN Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,

AN Blake J.A., Bradt D., Brusic V., Chothia C., Gough J.,

AN Blake J.A., Bradt D., Fletcher C.F., Forrest A., Gough J.,

AN Blake J.A., Bradt D., Hirokawa N., Jackson I.J., Jarvis E.D.,

AN Gasterland T., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,

Kanai A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,

AN Kanai A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,

AN Magashima T., Numata K., Okido T., Pavan M.J., Pertea G., Pesole G.,

AN Negashima T., Need J.C., Reed D.J., Reid J., Ramachandran S.,

AN Negashima T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,

AN Sandelin A., Schneider C., Semple C.A., Secou M., Shimada K.,

AN Schirler B., The C., Semple C.A., Secou M., Shimada K.,

AN Schirler B., The C., Semple C.A., Secou M., Shimada K.,

AN Schirler B., The C., Semple C.A., Secou M., Shimada K.,

AN Schirler B., The C., Semple C.A., Secou M., Shimada K.,

AN Schirler B., The C., Semple C.A., Secou M., Shimada K.,

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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUCLEOTIDE SEQUENCE [MRNA], FUNCTION, TISSUE SPECIFICITY, PHOSPHORYLATION, AND INTERACTION WITH EIF4E.
MEDLINE=9535483; PubMed=7629182; DOI=10.1074/jbc.270.31.18531; Lin T.-A., Kong X., Saltiel A.R., Blackshear P.J., Lawrence J.C. "Control of PHAS-I by insulin in 3T3-L1 addpcytee. Synthesis, degradation, and phosphorylation by a rapamycin-sensitive and mactivated protein kinase-independent pathway."; J. Biol. Chem. 270:18531-18538(1995).
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Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, BC064150; AAH64150.1; -; mRNA.
GO; GO:0008190; F:eukaryotic initiation factor 4E binding; IEA.
GO; GO:0045947; P:negative regulation of translational initia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
STRAIN=C57BL/6J; TISSUE=Embryo;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Euarchontoglires; Glires; Rodent Muroidea; Murilae; Murinae; Mus.
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10-OCT-2003 (Re
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10-OCT-2003 (Rel. 42, Created)
13-SEP-2005 (Rel. 48, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation updat
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C., Sempic
I., Taylor M.S.,
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Pred. No.
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RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Stapleton M., Ugdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Raha S.S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA RA Rakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA RA Rakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA RA Rakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA RA Rakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C. Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L., Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N., Hicozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K., Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S., Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I., Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A., Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J., Birney E., Hayashizaki Y.;
Birney E., Hayashizaki Y.;
Birney E., Hayashizaki Y.;
"Analysis of the mouse transcriptome based on functional annotation "Banalysis of the mouse transcriptome based on functional annotation "Nacing Color of Col
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and mouse cDNA sequences.";

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

-I- FUNCTION: Regulates eIF4E activity by preventing its assembly into the eIF4F complex. Mediates the regulation of protein translation by hormones, growth factors and other stimuli that signal through
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=22388257;
                                                                                                                                                                                                                                                    Ensembl; ENSMUSG00000031490; Mus musculus. MGI; MGI:103267; Eif4ebpl.
GO; GO:0005515; F:protein binding; IPI.
GO; GO:0030371; F:translation repressor ac
GO; GO:0030371; F:translation receptor signal;
GO; GO:0006286; P:insulin receptor signal;
GO; GO:0006446; P:regulation of translation
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EMBL; AK013033; BAB28612.1; -; mRNA.
EMBL; BC002045; AAH02045.1; -; mRNA.
                                                                                   PANTHER; PTHR12669; EIF4EBP; 1.
Pfam; PF05456; eIF_4EBP; 1.
Acetylation; Phosphorylation; Protein synthesis
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SIMILARITY: Belongs to the eIF4E-binding protein family.
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the MAP kinase pathway.

SUBUNIT: Nonphosphorylated EIF4EBP1 competes with EIF4G1/EIF4G3

interact with EIF4E; insulin stimulated MAP-kinase (MAPK1 and interact) phosphorylation of EIF4EBP1 causes dissociation of the complex allowing EIF4G1/EIF4G3 to bind and consequent initiation of translation. Rapamycin can attenuate insulin stimulation,
                                                                                                                                                                                                                                                             GO:0005515; F:protein binding; IPI.
GO:0030371; F:translation repressor activity; TAS.
GO:0008286; P:insulin receptor signaling pathway; IDA.
GO:0006446; P:regulation of translational initiation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE SPECIFICITY: Highest expression in fat cells. PTM: Phosphorylated on serine and threonine residues
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                                                                                                                                                                                                                        IPR008606;
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7; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                          ; EIF4EBP.
EIF4EBP; 1.
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RESULT 14
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Best Local S
Matches
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10-QCT-2003 (Rel. 42, Created)
13-SEP-2005 (Rel. 48, Last sequence update)
13-SEP-2005 (Rel. 48, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Eukaryotic translation initiation factor 4E-binding
(eIF4E-binding protein 1) (Phosphorylated heat- and
protein regulated by insulin 1) (PHAS-I).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4EBP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AND 97-116, PHOSPHORYLATION, AND TISSUE SPECIFICITY.
STRAIN-Sprague-Dawley; TISSUE-Adipocyte, and Skeletal muscle;
MEDLINE-94224815; PubMed-8170978;
Hu C., Pang S. V ... Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Euarchontoglires; Glires; Roden
Muroidea; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                        Sonenberg N., Lawrence J.C. Jr., "PHAS-I as a link between mitogen-activated translation initiation.";
Science 266:653-656(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                               Hu C., Pang S., Kong X., Velleca M., Lawrence J. "Molecular cloning and tissue distribution of PH target for insulin and growth factors."; proc. Natl. Acad. Sci. U.S.A. 91:3730-3734 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Name=Eif4ebp1;
EMBL; U05014; AAA86938 PIR; A55258; A55258.
                                                                                                                       <u>:</u>
                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=95025978; PubMed=7939721
                                                                                                                                                                                                                                                                                                                                                                                                                      FUNCTION, INTERACTION WITH EIF4E,
                                       removed
                                                                                            This
                                                                                                                                                                                                                                                                                                                                                                               Lin T.-A.,
                                                                                                                                                                                                                                                                                                                                                                                                            AND MAPKG,
                                                                                                                                                                          TISSUE SE
                                                                                                                                                                                                  FUNCTION: Regulates eIF4E activity by preventing its assembly into the eIF4F complex. Mediates the regulation of protein translation by hormones, growth factors and other stimuli that signal through the MAP kinase pathway.

SUBUNIT: Nonphosphorylated EIF4EBP1 competes with EIF4G1/EIFG3 to interact with EIF4E; insulin stimulated MAP-kinase (MAPK1 and MAPK3) phosphorylation of EIF4EBP1 causes dissociation of the complex allowing EIF4G to bind and consequent initiation, mediated translation. Rapamycin can attenuate insulin stimulation, mediated
                                                                                                                    to insulin, EGF and PDGF.
SIMILARITY: Belongs to the eIF4E-binding
                                                                                                                                              TISSUE SPECIFICITY: Expressed in all tissues examined; highest levels in fat and skeletal tissue, lowest levels in kidney. PTM: Phosphorylated on serine and threonine residues in respons
                                                                           Swiss-Prot entry is copyright. It is produced through a ceen the Swiss Institute of Bioinformatics and the EMBL
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                                                                  Bioinformatics
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12194
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S -> N (in Ref
                                                                    Institute.
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Pred. No.
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PHAS-I,
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                                                                                                                                                                                                                                                                                                                                                                                   Belsham G
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein 1 (4E-BP1)
acid-stable
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                                                        thie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              an
                                                                    restrictions
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                                                        statement
                                                                                              a collaboration
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SQ FITTER TO BE

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RESULT
4EBP1_H
    ALD ARRENT REPORTED TO THE PROPERTY OF THE PRO
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Best Local
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                                                                                    Phelan M., rann r
"Cloning of human r
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CONFLICT
CONFLICT
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MOD_RES
MUTAGEN
                                                                                                                                                                                                                                                                                                                                                                          TISSUB-Placenta;

MEDLINE=95021760; PubMed=7935836; DOI=10.1038/371762a0;

Pause A., Belsham G.J., Gingras A.-C., Donze O., Lin T.-A.,

Lawrence J.C. Jr., Sonenberg N.;

"Insulin-dependent stimulation of protein synthesis by phosphorylation of a regulator of 5'-cap function.";

Nature 371:762-767(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q13541; Q6IBN3;
10-OCT-2003 (Rel. 42, Created)
13-SEP-2005 (Rel. 48, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryotic translation initiation factor 4E-binding (eIF4E-binding protein 1) (Phosphorylated heat- and protein regulated by insulin 1) (PHAS-I).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PANTHER; PTHR12669; EIF4EBP; 1.
Pfam; PF05456; eIF_4EBP; 1.
Acetylation; Direct protein sequencing; Phosphorylation;
Protein synthesis inhibitor; Translation regulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      88
  NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA]
Ebert L., Schick M., Neubert P., Schat
"Cloning of human full open reading fr
                                                                                Submitted
                                                                                                                                                                             NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
Kalnine N., Chen X., Rolfs A., Halleck
                                                                                                                                                                                                                                         "Identification of multiple pancreatic cancer cells."; Submitted (JUN-2000) to the
                                                                                                                                                                                                                                                              pancreatic
                                                                                                                                                                                                                                                                                                                                           NUCLEOTIDE SEQUENCE [MRNA]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PHOSPHORYLATION.
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Eukaryota; Metazoa; C
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                                                                                                                                                           Koundinya M., Raphael J., Moreira
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||||||||
9 RIIYDRKFL 57
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                                                                                (MAY-2003)
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Euarchontoglires;
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Phosphoserine (by 'S->A: Decreases pho
and MAPK3. Ref. 1,
T -> P (in Ref. 1,
P -> I (in Ref. 1;
reading frames
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T -> P (in Ref. 1; A
P -> L (in Ref. 1; A
C449987B3DDEFB77 C
                                                                                                                                                         , Halleck A.,
eira D., Kelle
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                                                                                                                        ВВ
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by MAPK1 and MAPK3)
phosphorylation by
  Henze S., K
Gateway(TM)
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CRC64;
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                                                                                                                                                             L., Ei
                                                                                                                                                                                                                                                                                                                      N., Saito
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acid-stable
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                                                                                                                                                           Eisenstein
laer J., Lin
                                                                                                                     system
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                      Korn
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RC TISSUE-Colon, and Lung;

RX MEDLINE-22388257; PubMed-12477932; DOI=10.1073/pnas.242603899;

RX MEDLINE-22388257; PubMed-12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Alteschul S.F., Zeebberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Alteschul S.F., Zeebberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA HOpkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Stapleton M.J., UEdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Brownstein M.J., UEdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Brownstein M.J., McGernan K.J., Malek J.A., Gunaratne P.H.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Glbbs R.A.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Glbbs R.A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

"Generation and initial analysis of more than 15,000 full-length human

"Generation and initial analysis of more than 15,000 full-length human

RT and mouse cDNA sequences.";
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Submitted (JUN-2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 competition with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Haghighat A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Exploring proteomes and analyzing protein process spectrometric identification of sorted N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gevaert K., Goethals M., Martens L., Thomas G.R., Vandekerckhove J.;
                                                                                                                                                                                                                                    This Swiss-Prot entry is copyright. It is produced through
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=96091142;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nat. Biotechnol. 21:566-569(2003).
[7]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Repression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INTERACTIONS WITH EIF4E AND EIF4G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Platelet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROTEIN SEQUENCE OF 1-12, AND ACETYLATION
                                                                                                                                                                                                                                                                           mediated by FKBPs.

INTERACTION:

P06730:EIF4E; NbExp=2; IntAct=EBI-74090, EE
P06730:EIF4EL3; NbExp=1; IntAct=EBI-74090,
PTM: Phosphorylated on serine and threonine
to insulin, EGF and PDGF
SIMILARITY: Belongs to the eIF4E-binding px
                                                                                                                                                                                                                                                                                                                                                                                                             O'J. 14:5701-5709(1995).

PUNCTION: Regulates eIF4E activity by preventing its assembly int the eIF4F complex. Mediates the regulation of protein translation by hormones, growth factors and other stimuli that signal through the MAP kinase pathway.

SUBUNIT: Nonphosphorylated EIF4EBP1 competes with EIF4G1/EIF4G3 tinteract with EIF4E; insulin stimulated MAPKinase (MAPK1 and MAPK3) phosphorylation of EIF4EBP1 causes dissociation of the complex allowing EIF4G1/EIF4G3 to bind and consequent initiation of translation. Rapamycin can attenuate insulin stimulation,
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                                                                                                                                                                                                 European
AB044548; BAB1; BT007162; AAP3; CR456769; CAG3; CR456759; AAH00; BC058073; AAH5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             )1142; PubMed=8521827;
) Mader S., Pause A., Sonenberg N.;
of cap-dependent translation by 4E-binding with p220 for binding to eukaryotic initiat
                                                                                                                                                                           as its
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Bioinformatics
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                                                       BAB18650.1;
AAP35826.1;
CAG33050.1;
                    AAH04459.
AAH58073.
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                                                                                                                                                                             content
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S50866;

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DR IntAct; Q13541; -.

DR Ensembl; ENSG00000187840; Homo sapiens.

DR HGNC; HGNC; 3288; EIF4BBP1.

DR Reactome; Q13541; -.

DR MIM; 602223; -.

DR GO; G0:006445; P:regulation of translation; TAS.

DR GO; G0:006445; P:regulation of translation; TAS.

DR InterPro; IPR08606; EIF4BBP.

DR Pfam; PP05456; EIF4BBP; 1.

DR Pfam; PP05456; EIF 4BBP; 1.

DR Pfam; PP05456; EIF4BBP; 1.

Protein synthesis inhibitor; Translation regulation.

FT INIT MET 0 0 N-acetylserine (by MAPK1 and MAPK3) (By PT MOD_RES 64 64 Phosphoserine (by MAPK1 and MAPK3) (By PT MOD_RES 64 64 Phosphoserine (by MAPK1 and MAPK3) (By PT MOD_RES 64 64 Phosphoserine (by MAPK1 and MAPK3) (By PT MOD_RES 64 64 Phosphoserine (by MAPK1 and MAPK3) (By PT MOD_RES 64 64 Phosphoserine (by MAPK1 and MAPK3) (By PT MOD_RES 64 64 Phosphoserine (by MAPK1 and MAPK3) (By PT MOD_RES 64 64 Phosphoserine (by MAPK1 and MAPK3) (By PT MOD_RES 64 64 Phosphoserine (by MAPK1 and MAPK3) (By PT MOD_RES 64 64 Phosphoserine (by MAPK1 and MAPK3) (By PT MOD_RES 64 64 Phosphoserine (by MAPK1 and MAPK3) (By PT MOD_RES 64 64 Phosphoserine (by MAPK1 and MAPK3) (By PT MOD_RES 64 64 Phosphoserine (by MAPK1 and MAPK3) (By PT MOD_RES 64 64 Phosphoserine (by MAPK1 and MAPK3) (By PT MOD_RES 64 64 Phosphoserine (by MAPK1 and MAPK3) (By PT MOD_RES 64 64 Phosphoserine (by MAPK1 and MAPK3) (By PT MOD_RES 64 64 Phosphoserine (by MAPK1 and MAPK3) (By PT MOD_RES 64 64 Phosphoserine (by MAPK1 and MAPK3) (By MAPK1 and MAPK3) (By PT MOD_RES 64 64 Phosphoserine (by MAPK1 and MAPK3) (By MAPK1 and MAPK3) (By PT MOD_RES 64 64 Phosphoserine (by MAPK1 and MAPK3) (By MAPK1 and MAPK1 and MAPK3) (By MAPK1 and MAPK1 and MAPK1 and MAPK1 and MAPK1 and MAPK1
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Sequence Sequence Sequence

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Post-processing: Minimum Match 10% Maximum Match 100
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re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.
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1 RIIYDRKFLX 10
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1: /cgn2_6/ptcdata/1/iaa/5_COMB.pep:*

2: /cgn2_6/ptcdata/1/iaa/6_COMB.pep:*

3: /cgn2_6/ptcdata/1/iaa/H_COMB.pep:*

4: /cgn2_6/ptcdata/1/iaa/PCTUS_COMB.pep:*

5: /cgn2_6/ptcdata/1/iaa/RE_COMB.pep:*

5: /cgn2_6/ptcdata/1/iaa/RE_COMB.pep:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query
Match Length
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US-08-869-733-1
US-10-09-215-063-1
US-10-096-703-1
US-09-949-016-7744
US-08-869-733-3
US-09-215-063-4
US-09-215-063-4
US-09-215-063-4
US-09-949-016-7860
US-08-465-995A-2
US-08-465-995A-2
US-08-465-994C-2
US-08-465-994C-2
US-08-966-145-2
US-08-966-145-2
US-08-96-145-2
US-09-107-532A-3743
US-09-107-532A-3743
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US-08-869-733-1
                                                                          US-08-869-733-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Applic Patent No. 5955278
                                                                                                                                                                                                                                                                          COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION NUMBER: US/08/869,733
FILING DATE: Herewith
CLASSIFICATION INUMBER: US/08/869,733
FILING DATE: Herewith
CLASSIFICATION DATA:
APPLICATION NUMBER: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
APTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 9F-0310 US
REFERENCE/DOCKET NUMBER: PF-0310 US
TELEPHONE: 415-855-0555
TELEPHONE: 415-855-0555
        Matches
                                          Query Match
                                                                                                                                                                                 TELEX:
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
SEQUENCE HARACTERISTICS:
1-ENGTH: 100 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Hawkins, Phillip R.
TITLE OF INVENTION: NEW TRANSLATIONAL REGULATOR
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: sinc
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: BSTMNOTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET:
                       Local Similarity
                                                                                                                                                                                                                                                                   TELEFAX: 415-845-4166
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                                                                                          CLONE:
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                                                                                            805296
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3174 Porter Drive
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          Conservative
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     97.9%; Scu.
100.0%; Pr
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US-09-270-775-50854
US-09-270-767-50854
US-09-854-122-43
US-09-854-122-43
US-09-854-767-15
US-09-158-767-16
US-09-158-767-16
US-09-158-767-17
US-09-158-767-18
US-09-158-767-18
US-09-158-767-18
US-09-131-794-15
US-09-713-794-15
US-09-713-794-18
          b; Score 46; DB
b; Pred. No. 0.1
0; Mismatches
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0.11;
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Minimum Maximum

88

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Database

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US-09-215-063-1
                                                                                           Sequence 1, Application US/10096703
Patent No. 6677126
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/09215063
Patent No. 6365714
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: PastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/215,063
FILING DATE: 17-Dec-1998
CLASSIFICATION: «Unknown»
PRIOR APPLICATION NUMBER: 08/869,733
APPLICATION NUMBER: 08/869,733
FILING DATE: «Unknown»
APPLICATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: 96,749
REFERENCE/DOCKET NUMBER: PF-0310 US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                   y Match 97.9%; So
Local Similarity 100.0%; I
hes 9; Conservative 0;
                  APPLICANT: Hillman, Jennifer L.
Hawkins, Phillip R.
TITLE OP INVENTION: NEW TRANSLATIONAL REGULATOR NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          IMMEDIATE SOURCE:
LIBRARY: BSTMNOT01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Hillman, Jennifer L.
Hawkins, Phillip R.
TITLE OF INVENTION: NEW TRANSLATIONAL REGULATOR NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                      1 RIIYDRKFL 9
||||||||
37 RIIYDRKFL 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 100 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                            CLONE: 805296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEX: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
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s; Pred. No. 0.1
0; Mismatches
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FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-00-031,498

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FASTSEQ for Windows Version 4.0

SEQ ID NO 7744

LENGTH: 118

TYPE: PRT
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Best Local Similarity
Watches 9; Conserve
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                                         ) ORGANISM: Human
US-09-949-016-7744
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 7744, Application US/09949016 Patent No. 6812339
                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
  Query Match
                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/215,063

FILING DATE: <UNKnown>
ATTORNEY/AGENT INFORMATION:

NAME: Billings, Lucy J.

REGISTRATION NUMBER: 36,749

REFERENCE/DOCKET NUMBER: PF-0310 US

TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
OPERATING SYSTEM: DOS
OPERATING SYSTEM: DOS
OPERATING SYSTEM: DOS
OPERATION DATA:
APPLICATION NUMBER: US/10/096,703
FILING DATE: 12-Mar-2002
CLASSIFICATION: Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LIBRARY: BSTMNOT01
CLONE: 805296
SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: 15
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          37 RIIYDRKFL 45
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STREET: 3174 Porter Drive
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 100 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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  97.98;
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Pred. No.
  Score 46;
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0.11;
  DB 2;
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Length 118;
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CORRESPONDENCE ADDRESS:

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                                                                                                       RESULT 6
US-08-869-733-4
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Patent No. 5958278
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Hawkins, Phillip R.
TITLE OF INVENTION: NEW TRANSLATIONAL REGULATOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local
Matches
           Sequence 4, Application US/08869733
Patent No. 5955278
GENERAL INFORMATION:
APPLICANT: Hawkins, Phillip R.
TITLE OF INVENTION: NEW TRANSLAY
                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOPTWARE: FASUSSO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/869,733
FILING DATE: Herewith
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNMBER:
FILING DATE:
FILING DATE:
                                                                                                                                                                                                                                                                                       STRANGE 1110-
TOPOLOGY: 1110-
IMMEDIATE SOURCE:
LIBRARY: GenBank
                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
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NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 3174 PO:
CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Incyte Pharmaceuticals, Inc. STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 120 amino acids
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                                                                                                                                                                   51 RIIYDRKFL 59
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9; Conservative
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                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                               97.9%; Score 46; 100.0%; Pred. No.
            Jennifer L.
Phillip R.
NEW TRANSLATIONAL REGULATOR
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; Mismatches
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                                                                                                                                                                                                                                               DB 1;
0.13;
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RESULT 7
US-09-215-063-3
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Patent No. 6365714
GENERAL INFORMATION:
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Best Local Similarity
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OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/869,733
FILING DATE: Herewith
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MEDIUM TYPE: Diskett
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LIBRARY: GenBank
CLONE: 1658516
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NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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STRANDEDNESS: si
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              COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTEM: DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/215,063
FILING DATE: 17-Dec-1998
CLASSIFICATION: <Unknown>
                                                                                                                                       ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS: Parmaceuticals, Inc
                                                                                                                                                                                                                                                                                                                  Hawkins, Phillip R.
TITLE OF INVENTION: NEW TRANSLATIONAL REGULATOR
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Hillman, Jennifer L.
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US-09-215-063-4
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Patent No. 6365714
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
Hawkins, Phillip R.
TITLE OF INVENTION: NEW TRANSLATIONAL REGULATOR
NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 97.9%; Score 46; DB 2; Best Local Similarity 100.0%; Pred. No. 0.13; Matches 9; Conservative 0; Mismatches
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INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                 TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                   PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/869,733

FILING DATE: <UNknown>
ATTORNEY/AGENT INFORMATION:

NAME: Billings, Lucy J.

REGISTRATION NUMBER: 36,749

REGERENCE/DOCKET NUMBER: PF-0310 US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-855-555
                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/215,063
FILING DATE: 17-Dec-1998
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc
STREET: 3174 Porter Drive
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
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STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
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REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0310 US
LENGTH: 120 amino acids
TYPE: amino acid
STRANDEDNESS: single
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CLONE: 561632
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LIBRARY: GenBank
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CLONE: 561632
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SEQUENCE DESCRIPTION: SEQ ID NO:
US-10-096-703-3
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Patent No. 6677126
GENERAL INFORMATION:
                                                                Matches
                                                                                Query Match
Best Local :
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Best Local S
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INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: FastSEQ for Windows Ver:
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/10/096,703
FILING DATE: 12-Mar-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
                                                                                                                                                                                                                                                                                                                            NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0310 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEPAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: NEW TRANSLATIONAL REGULATOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Hillman,
51 RIIYDRKFL 59
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                                1 RIIYDRKFL 9
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Similarity 100.0%; Pred. No. 0.13;
9; Conservative 0; Miamatoho-
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                                                                                Similarity
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CLONE: 1658516
                                                                                                                                                                                                                               STRANDEDNESS: single
                                                                                                                                                                                                                                             TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: DOS SOFTWARE: FastSEQ for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM Compatible
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                                                                Conservative
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                                                                                97.9%; Score 46; DB 2; 100.0%; Pred. No. 0.13;
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                                                                Mismatches
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RESULT 10

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US-10-096-703-4
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Patent No. 6677126
GENERAL INFORMATION:
Sequence 7860, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/231,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
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Best Local Similarity 100.0%;
Matches 9; Conservative (
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INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: amino acid
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FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0310 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
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OPERATING SYSTEM: DOS
SOPTMARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
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Hawkins, Phillip R.
TITLE OF INVENTION: NEW TRANSLATIONAL REGULATOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 94304
COMPUTER READABLE FORM:
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CORRESPONDENCE ADDRESSE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LIBRARY: GenBank
CLONE: 1658516
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                       51 RIIYDRKFL 59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/10/096,703
FILING DATE: 12-Mar-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: CA
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Best Local Similarity
Whiches 9; Conserve
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; ORGANISM: Human
US-09-949-016-7860
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RESULT 13
US-08-465-995A-4
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SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 7860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Patent No. 5660980
                                                                                                                                      Best
                                                                                                                                                    Query Match
                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: ASCIL DOS/TEXT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,995A
FILING DATE: 06-UN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Robert Berliner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                            TELEFAX: 213/977-1003
INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 898 amino acids
                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 20,121
REFERENCE/DOCKET NUMBER: 19
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 90012-2628
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                 TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Myron F. Goodman
APPLICANT: Linda J. Reha-Krantz
TITLE OF INVENTION: METHODS FOR IDENTIFYING AND ISOLATING
TITLE OF INVENTION: VARIANT T4 POLYMERASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 201 No. 5660980th Figueroa Street, CITY: Los Angeles STATE: California
                                                                                                                 y Match 78.7%;
Local Similarity 75.0%;
hes 6; Conservative
                                                                                                                                                                                                                                                                                                         TELEPHONE:
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                                                           2 IIYDRKFL 9
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99 IVYDRKFV 106
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Sequence 4, Application US/08465995A Patent No. 5660980 GENERAL INFORMATION:

APPLICANT:
APPLICANT:

Myron F. Goodman Linda J. Reha-Krantz

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RESULT 14
US-08-465-994C-2
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Best Local Similarity 75.0%;
Matches 6; Conservative
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INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
SEQUENCE SHARACTERISTICS:
SEQUENCE SHARACTERIS
                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: ASCII DOS/TEXT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,994C
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
APPLICATION: 435
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ATTORNEY/AGENT INFORMATION:
NAME: MARGARET A. CHURCHILL
REGISTRATION NUMBER: 39,944
REFERENCE/DOCKET NUMBER: 1920
TELECOMMUNICATION INFORMATION:
TELEPHONE: 213/977-1001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NERAL INFORMATION F. GOUDERAND APPLICANT: MYRON F. GOUDERAND APPLICANT: LINDA L. REHA-KRANTZ

***POPLICANT: LINDA L. REHA-KRANTZ
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,995A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Robbins, Berliner & Carson, LLP
STREET: 201 No. 5928919th Figueroa Street,
CITY: Los Angeles
STATE: California
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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NAME: Robert Berliner
REGISTRATION NUMBER: 20,121
REFERENCE/DOCKET NUMBER: 19
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ADDRESSEE: Robbins, Berliner & Carson, LLP
STREET: 201 No. 5660980th Figueroa Street, Suite 500
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CITY: LOS Angeles
STATE: California
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CLASSIFICATION:
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|VYDRKFV 106
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Search completed: November 29, 2005, 23:04:22 Job time: 24.8636 secs
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Best Local Similarity
Matches 6; Conserv
                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Patent No. 5928919
GENERAL INFORMATION:
APPLICANT: MYRON F. GOODMAN
APPLICANT: LINDA L. REHA-KRANTZ
TITLE OF INVENTION: VARIANT DNA POLYMERASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 4,
                                                                                                                                              Query Match
                                                                                                                                                                                                                                     TELEPHONE: 213/977-1001
TELEFAX: 213/977-1003
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 898 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: BM PC COMPATIBLE
OPERATING SYSTEM: ASCII DOS/TEXT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,994
                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 39,944
REFERENCE/DOCKET NUMBER: 19
TELECOMMUNICATION INFORMATION:
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ADDRESSEE: Robbins, Berliner & Carson, LLP
STREET: 201 No. 5928919th Figueroa Street,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS LENGTH: 898 amino aci
                                                                                                                                                                                              MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: MARGARET A. CHURCHILL
REGISTRATION NUMBER: 39,944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                    Local
                                                                                                                                                                                                                              TYPE:
                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 06-JUN
CLASSIFICATION: 435
                                                                                                                                                                                                            TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Los Angeles
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                                                                                                                  l Similarity
6; Conserv
                                                                                      2 IIYDRKFL 9
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amino acid
XGY: linear
                                                                                                                                                                                                           amino acid
GY: linear
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|VYDRKFV 106
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                                                                                                                   Conservative
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75.0%;
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75.0%;
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                                                                                                                                   Score 37;
Pred. No.
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Pred. No.
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No.
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Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Database
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence:
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  202221175
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                    Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq length: 0
seq length: 2000000000
  protein search, using
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             November 29, 2005, 22:52:34 ; Search time 77.9545 Seconds (without alignments) 53.599 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1867569 seqs, 417829326 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 RIIYDRKFLX 10
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1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*

6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*
  GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd
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  63
9
16
128
898
105
977
1679
1679
1679
223
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US-10-353-929-14
US-09-973-473-6
US-09-973-473-7
US-09-973-473-8
US-10-996-763A-416
US-10-631-467-1617
US-10-353-929-48
US-10-955-300-1267
US-10-966-703-3
US-10-966-703-3
US-10-966-703-4
US-09-925-301-1164
US-09-925-301-1164
US-09-9273-473-15
US-10-425-115-272454
US-10-425-115-272454
US-10-99-143-8286
US-11-997-143-8286
US-11-997-143-8286
US-10-9973-473-17
US-10-973-473-17
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  Sequence
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  15, Appl
68, Appl
197, Appl
272454,
272448,
272448,
8286, Ap
8286, Ap
16, Appl
17, Appl
17, Appl
261205, A
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6, Appli
7, Appli
8, Appli
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416, Appli
1617, Ap
1617, Appli
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1617, Appli
1617, Appli
1617, Appli
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                                                                                                                                                                                                                                                                                                                                            US-09-973-473-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Homo sapiens
US-09-973-473-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 7
LENGTH: 16
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 7, Application US/09973473 Publication No. US20030041341A1 GENERAL INFORMATION:
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Best Local
APPLICANT: SONENBERG, Nahum
APPLICANT: TREMBLAY, MiChel
APPLICANT: TREMBLAY, MiChel
APPLICANT: TSUKIAYAMA-KOHARA, KYOKO
TITLE OF INVENTION: NON-HUMAN TRANSGENIC ANIMAL WHOSE GERM CELLS AND
TITLE OF INVENTION: SOMATIC CELLS CONTAIN A KNOCKOUT MUTATION IN DNA
TITLE OF INVENTION: ENCODING 4E-BP1
FILE REFERENCE: 514012000400
CURRENT APPLICATION NUMBER: US/09/973,473
CURRENT FILING DATE: 2001-10-03
PRIOR APPLICATION NUMBER: PCT/CA00/00388
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: 60/128,559
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APPLICANT: TREMBLAY, MISCHEI
APPLICANT: TREMBLAY, MISCHEI
APPLICANT: TSUKIAYAMA-KOHARA, KYOKO
TITLE OF INVENTION: NON-HUMAN TRANSCENIC ANIMAL WHOSE GERM CEILS AND
TITLE OF INVENTION: SOMATIC CELLS CONTAIN A KNOCKOUT MUTATION IN DNA
TITLE OF INVENTION: SOMATIC CELLS CONTAIN A KNOCKOUT MUTATION IN DNA
FILE REFERENCE: 514012000400
CURRENT APPLICATION NUMBER: US/09/973,473
CURRENT APPLICATION NUMBER: US/09/973,473
CURRENT FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: 60/128,559
PRIOR APPLICATION NUMBER: 60/128,559
PRIOR FILING DATE: 2090-04-07
PRIOR FILING DATE: 1999-04-09
PRIOR FILING DATE: 1999-04-09
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PRIOR FILING DATE: 2000-02-02
NUMBER OF SEQ ID NOS: 27
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PRIOR FILING DATE: 2000-02-02
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 100 tes 9; Conservative
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y 100.0%; Pre
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Pred. No.
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0.044;
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; TYPE: PRT ; ORGANISM: Homo sapiens US-09-973-473-8
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US-10-096-703-1
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PRIOR APPLICATION NUMBER: 60/179,743
PRIOR FILING DATE: 2000-02-02
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO
Query Match
Best Local Similarity
Matches 9; Conserv
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Publication No. US20020132330A1
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer
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Matches 9; Conserv
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                                                                                                                                                                                                                                  TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH:
                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/215,063
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTMARE: FASTEM: DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/096,703
FILING DATE: 12-Mar-2002
CLASSIFICATION: <Unknown>
                                                                                                                                             TOPOLOGY: 1in
                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: PF-0310 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
                                                                                           SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: NEW TRANSLATIONAL REGULATOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 RIIYDRKFL 9
                                                                                                                                                                              LENGTH: 100 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                LIBRARY: BSTMNOT01
CLONE: 805296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Diskette
     Conservative
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Hawkins, Phillip R.
                                                                                                                                                               linear
                      97.9%;
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                      Score 46; Pred. No.
     0;
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       Mismatches
                      DB 4;
0.29;
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                                    Length 100;
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1 RIIYDRKFL 9

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FILE REFERENCE: 660088.465
CURRENT APPLICATION NUMBER: US/10/408,765A
CURRENT FILING DATE: 2003-04-04
NUMBER OF SEQ ID NOS: 3077
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 416
LENGTH: 100
TYPE: PRT
ORGANISM: Homo sapiens
US-10-408-765A-416
                                                                                                                                                                                                                                                                                                             FILE REFERENCE: 3462.1005-000
CURRENT APPLICATION NUMBER: US/10/631,467
CURRENT FILING DATE: 2003-07-31
PRIOR APPLICATION NUMBER: UP 2003-077212
PRIOR FILING DATE: 2003-03-20
PRIOR APPLICATION NUMBER: UP 2002-229312
PRIOR FILING DATE: 2002-08-06
NUMBER OF SEQ ID NOS: 2086
SOPTWARE: Patentin version 3.1
SEQ ID NO 1617
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US-10-631-467-1617
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RESULT 8
US-10-353-929-48
; Sequence 48, Application US/10353929
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US-10-631-467-1617
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Best Local Similarity
Thes 9; Conserva
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Publication No. US20040101874A1
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Best Local Similarity
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APPLICANT:
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APPLICANT:
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APPLICANT: Fahy, Eoin D.
APPLICANT: Zhang, Bing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Warnock, Dale E.
TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Genox Research Inc.
TITLE OF INVENTION: Method for testing for broncheal asthma, or chronic obstructive
TITLE OF INVENTION: disease
                                                                                                                                                                                                                                                                                                   LENGTH: 117
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Taylor, Steven W.
Glenn, Gary M.
                                                                                               RIIYDRKFL 58
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ilarity 100.0%;
Conservative (
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                                                                                                                                                                                         97.9%; Score 46; DB 5; 100.0%; Pred. No. 0.33;
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PRIOR APPLICATION NUMBER: JP P2000-231814
PRIOR FILING DATE: 2003-01-30
PRIOR FILING DATE: 2000-07-31
NUMBER OF SEQ ID NOS: 197
SOFTWARE: PatentIn version 3.1
SEQ ID NO 48
LENGTH: 118
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US-10-631-467-917
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Homo sapiens 
US-10-631-467-917
                                                                                                                                                                                                                                RESULT 10
US-09-925-300-1267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 917, Applic Publication No. US20 GENERAL INFORMATION:
                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Craig Rosen,
APPLICANT: Steve Ruben
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 917
LENGTH: 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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                                                                                                                                                                                                                                                                                                                                                                                           Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: ITOH, Kyogo
TITLE OF INVENTION: Tumor antigen
FILE REFERENCE: GP01-1024
CURRENT APPLICATION NUMBER: US/10/353,929
CURRENT FILING DATE: 2003-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: JP 2003-077212
PRIOR FILING DATE: 2003-03-20
PRIOR APPLICATION NUMBER: JP 2002-229312
PRIOR FILING DATE: 2002-08-06
NUMBER OF SEQ ID NOS: 2086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Genox Research Inc.
TITLE OF INVENTION: Method for testing for broncheal asthma, or chronic obstructive $
TITLE OF INVENTION: disease
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies FILE REFERENCE: PA101
CURRENT APPLICATION NUMBER: US/09/925,300
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05988
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: disease
FILE REFERENCE: 3462.1005-000
CURRENT APPLICATION NUMBER: US/10/631,467
CURRENT FILING DATE: 2003-07-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn version 3.1
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ORGANISM: Homo sapiens
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Local Similarity 100.0%; P.
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o. US20050208496A1
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Pred. No.
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Sequence 3, Application US/10096703

Publication No. US20020132330A1

GENERAL INFORMATION:

APPLICANT: Hillman, Jennifer L.

Hawkins, Phillip R.

TITLE OF INVENTION: NEW TRANSLATIONAL REGULATOR

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSE: Incyte Pharmaceuticals, Inc.

STREET: 3174 Porter Drive

CTTY: Palo Alto
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                                                                                                                                    US-10-096-703-3
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US-10-096-703-3
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US-09-925-300-1267
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SEQ ID NO 1267
LENGTH: 119
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                                                                                    Best Local
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SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                         TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                           NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0310 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/215,063
FILING DATE: «Unknown»
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 94304
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
                                                                                                                                                        SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                        IMMEDIATE SOURCE:
51
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                                                                                    Similarity
                                RIIYDRKFL 9
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RIIYDRKFL 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/10/096,703 FILING DATE: 12-Mar-2002 CLASSIFICATION: «Unknown»
                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
                                                                                                                                                                      LIBRARY: GenBank CLONE: 561632
                                                                                                                                                                                                                                                                                                                                               TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Diskette
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                                                                                                                                                                                                                          TOPOLOGY: linear
                                                                                                                                                                                                                                                                          LENGTH: 120 amino acids
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                                                                    Conservative
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                                                                                  97.9%; Score 46; DB 4; Length 120; 100.0%; Pred. No. 0.34;
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US-09-925-301-1164
; Sequence 1164, Application US/09925301
; Patent No. US20020052308A1
; GENERAL INFORMATION:
TITLE OF INVENTION: Nucleic Acids, Proteins and Ant
FILE REFERENCE: PA106
; CURRENT APPLICATION NUMBER: US/09/925,301
; CURRENT APPLICATION NUMBER: US/09/925,301
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: FOT/US00/05882
; PRIOR FILING DATE: 2000-03-08
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR APPLICATION NUMBER: 60/124,270
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Best Local
NUMBER OF SEQ ID NOS: 1694
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INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 09/215,063
FILING DATE: «Unknown»
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REGISTRATION NUMBER: PF-0310 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/10/096,703
PILING DATE: 12-Max-2002
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLONE: 1658516
SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IMMEDIATE SOURCE:
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TITLE OF INVENTION: NEW TRANSLATIONAL REGULATOR
                                                                                                                                                                                                                                                                                                                                  51 RIIYDRKFL 59
                                                                                                                                                                                                                                                                                                                                                       1 RIIYDRKFL 9
                                                                                                                                                                                                                                                                                                                                                                                                           Similarity 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 120 amino acids TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
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Pred. No. 0.34;
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RESULT 15
US-10-353-929-15
US-10-353-929-15
Sequence 15, Application US/10353929
Publication No. US20030175288A1
GENERAL INFORMATION:
APPLICANT: ITOH, Kyogo
TITLE OF INVENTION: Tumor antigen
FILE REFERENCE: GP01-1024
CURRENT FILING DATE: 2003-01-30
PRIOR APPLICATION NUMBER: US/10/353,929
CURRENT PILING DATE: 2003-01-30
PRIOR PILING DATE: 2007-07-31
NUMBER OF SEQ ID NOS: 197
SOFTWARE: PatentIn version 3.1
SEQ ID NO 15
LENGTH: 0
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US-10-425-115-251396
(S-10-425-115-251396, Application US/10425115
; Sequence 251396, Application US/10425115
; Publication No. US20040214272A1
; Publication No. US20040214272A1
; GENERAL INFORMATION:
    APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(5)222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
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; ORGANISM: Homo sapiens
US-09-925-301-1164
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SEQ ID NO 1164
LENGTH: 138
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SEQ ID NO 251396
LEUGTH: 63
TYPE: PRT
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Best Local Similarity 100.0%;
Matches 9; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 89.4%; Score 42; DB 4; Length 63; Best Local Similarity 88.9%; Pred. No. 1.1; Matches 8; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Zea mays
FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(63)
OTHER INFORMATION: unsure at all Xaa locations
                                                      LENGTH: 9
TYPE: PRT
ORGANISM: Artificial
OTHER INFORMATION: Designed peptide having an ability to activate HLA-A2 restricted OTHER INFORMATION: Cytotoxic T lymphocytes
                                               FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 RIIYDRKFL 9
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9 RIIYERKFL 17
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US-10-353-929-15
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Query Match 87.2%; Score 41; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps
Qy 2 IIIVDRKFL 9
Db 1 IIVDRKFL 8
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Search completed: November 29, 2005, 23:10:28
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Minimum
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     protein search, using
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1: /cgn2_6/ptodata/2/pubpaa/USIO_NEW_PUB.pep:*

2: /cgn2_6/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*

3: /cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*

4: /cgn2_6/ptodata/2/pubpaa/USO9_NEW_PUB.pep:*

5: /cgn2_6/ptodata/2/pubpaa/USO9_NEW_PUB.pep:*

6: /cgn2_6/ptodata/2/pubpaa/USO9_NEW_PUB.pep:*

7: /cgn2_6/ptodata/2/pubpaa/USI1_NEW_PUB.pep:*

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Copyright (c) 1993 - 2005 Compugen Ltd.
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US-11-022-562-228
US-10-793-626-3174
US-10-821-234-915
US-10-821-234-915
US-10-821-234-1581
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Sequence 83, Appl Sequence 82, Appl Sequence 82, Appl Sequence 140, App Sequence 119, App Sequence 228, Appl Sequence 2774, App Sequence 3174, App Sequence 3174, App Sequence 1581, App Sequence 1582, App Sequence 1581, App Sequence 1683, App Sequence 16, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 13, Appl Sequence 14, Appl Sequence 13, Appl Sequence 14, Appl Sequence 15, Appl Sequence 17, Appl Sequence 18, Appl Sequence 19, Appl Sequence 17, Appl Sequence 212, Appl Sequence 212, Appl Sequence 212, Appl Sequence 212, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                    Description
   Sequence 141, Application US/10667295

Publication No. US20050257293A1

GENERAL INFORMATION:
APPLICANT: Mascia, Peter
TITLE OF INVENTION: BIOLOGICAL CONTAINMENT SYSTEM
FILE REFERENCE: 11696-047001
CURRENT APPLICATION NUMBER: US/10/667,295
CURRENT FILING DATE: 2003-09-17
PRIOR APPLICATION NUMBER: US 60/411,823
PRIOR FILING DATE: 2002-09-17
NUMBER OF SEQ ID NOS: 263
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 141
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US-10-667-295-141
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les 5; Conserv
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Sequence 23, Appi	2 6			109	Sequence 38, Appl	,		Sequence 2388, Ap			. 4	332,	4.	Sequence 366, App	Sequence 1/9, App	7816,	4		Sequence 161, App

ALIGNMENTS

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TYPE: PRT
ORGANISM: Arabidopsis thaliana
FEATURE:
NAME/KEY: VARIANT
LOCATION: (1)...(433)
OTHER INFORMATION: Ceres Seq. ID
US-10-667-295-83
                                                                                                                                                                                                                                                                                                                                                                  RESULT 1
US-10-667-295-83
; Sequence 83, Application US/10667295
; Publication No. US20050257293A1
; GENERAL INFORMATION:
                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 263
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 83
                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/10/667,295
CURRENT FILING DATE: 2003-09-17
PRIOR APPLICATION NUMBER: US 60/411,823
PRIOR FILING DATE: 2002-09-17
                                                                                                                                                                                                                                                                                                                          APPLICANT: Mascia, Peter
TITLE OF INVENTION: BIOLOGICAL CONTAINMENT
FILE REFERENCE: 11696-047001
Conservative
                68.1%;
62.5%;
                Score 32;
Pred. No.
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 Mismatches
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                                                                                     12558792
                DB 1;
7.2;
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 0,
                                Length 433;
   Indels
   0
   Gaps
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TITLE OF INVENTION: BIOLOGICAL CONTAINMENT SYSTEM
FILE REFERENCE: 11696-047001
CURRENT APPLICATION NUMBER: US/10/667,295
CURRENT FILING DATE: 2003-09-17
PRIOR PELICATION NUMBER: US 60/411,823
PRIOR FILING DATE: 2002-09-17
NUMBER OF SEQ ID NOS: 263
SOPTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 82
LENGTH: 505
TYPE: PRT
                                                                                                                APPLICANT: MASCIA, PETER
TITLE OF INVENTION: BIOLOGICAL CONTAINMENT SYSTEM
FILE REFERENCE: 11696-047001
CURRENT APPLICATION NUMBER: US/10/667,295
CURRENT FILING DATE: 2003-09-17
PRIOR APPLICATION NUMBER: US 60/411,823
PRIOR FILING DATE: 2002-09-17
NUMBER OF SEQ ID NOS: 263
SOFTWARE: PASTSEQ for Windows Version 4.0
SEQ ID NO 140
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Best Local Similarity
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FEATURE:

NAME/KEY: VARIANT
LOCATION: (1)...(434)
OTHER INFORMATION: Ceres Seq. ID no. 13531808
US-10-667-295-141
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; NAME/KEY: VARIANT
; LOCATION: (1)...(505)
; OTHER INFORMATION: Ceres Seq. ID no. 12558791
US-10-667-295-82
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Matches
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Publication No. US20050257293A1
GENERAL INFORMATION:
APPLICANT: Mascia, Peter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
ORGANISM: Glycine max
FEATURE:
NAME/KEY: VARIANT
LOCATION: (1)...(506)
OTHER INFORMATION: Ceres Seq. ID no. 13531807
                                                                                              TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Arabidopsis thaliana
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                                                                                                          ENGTH: 506
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Similarity 62.5%;
5; Conservative
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o. US20050257293A1
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62.5%;
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Pred. No. 8.3;
3; Mismatches
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APPLICANT: MASCIA, Peter
TITLE OF INVENTION: BIOLOGICAL CONTAINMENT SYSTEM
FILE REFERENCE: 11696-047001
CURRENT APPLICATION UNMBER: US/10/667,295
CURRENT FILING DATE: 2003-09-17
PRIOR APPLICATION NUMBER: US 60/411,823
PRIOR FILING DATE: 2002-09-17
NUMBER OF SEQ ID NOS: 263
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 139
LENGTH: 526
TWORE: DET
                                                                                                                                                                                      APPLICANT: MASCIA, Peter
TITLE OF INVENTION: BIOLOGICAL CONTAINMENT SYSTEM
FILE REFERENCE: 11696-047001
CURRENT APPLICATION UNMBER: US/10/667,295
CURRENT FILING DATE: 2003-09-17
PRIOR APPLICATION NUMBER: US 60/411,823
PRIOR FILING DATE: 2002-09-17
NUMBER OF SEQ ID NOS: 263
SOPTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 81
SEQ ID NO 81
Query Match
Best Local Similarity
Watches 5; Conserve
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Best Local Similarity
Watches 5; Conserve
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; OTHER INFORMATION: Ceres Seq.
US-10-667-295-139
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                                                                            US-10-667-295-81
                                                                                                                                                                                                                                                                                                                                                     Sequence 81, Application US/10667295 Publication No. US20050257293A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Publication No. US200 GENERAL INFORMATION:
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Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 139,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                      TYPE: PRT
ORGANISM: Arabidopsis thaliana
FEATURE:
NAME/KEY: VARIANT
IOCATION: (1)...(534)
OTHER INFORMATION: Ceres Seq. ID no. 12558790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
NAME/KEY: VARIANT
LOCATION: (1)...(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Glycine max
                                                                                                                                                                                     ENGTH:
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o. US20050257293A1
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              Conservative
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                            68.1%;
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              3; Mismatches
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Pred. No.
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                            Score 32; I
Pred. No. 8.
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Pred. No. 8.4;
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TYPE: PRT
; ORGANISM: Bacillus circulans
US-11-065-943-52
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US-11-022-562-228
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RESULT 9
US-10-793-626-2774
; Sequence 2774, Application US/10793626
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                                                                                                                                                        Query Match
Best Local Similarity
S; Conserve
                                                                                                                                                                                                                                                      ; TYPE: PRT ; ORGANISM: Clostridium difficile US-11-022-562-228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:

APPLICANT: JESTIN, JEAN-LUC

APPLICANT: VICHIER-GUERRE, SOPHIE

APPLICANT: VICHIER-GUERRE, SOPHIE

APPLICANT: FERRIS, STEPHANE

TITLE OF INVENTION: METHODS FOR OBTAINING THERMOSTABLE ENZYMES, DNA POLYMERASE I

TITLE OF INVENTION: VARIANTS FROM THERMUS AQUATICUS HAVING NEW CATALYTIC ACTIVITIES,

TITLE OF INVENTION: METHODS FOR OBTAINING THE SAME, AND APPLICATIONS OF THE SAME

FILE REFERENCE: 266426USOXCIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 228, Application US/11022562 Publication No. US20050249742A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 340
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 228
LENGTH: 396
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn version 3.3 SEQ ID NO 52
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CURRENT FILING DATE: 2005-02-25
PRIOR APPLICATION NUMBER: US 10/787,219
PRIOR FILING DATE: 2004-02-27
NUMBER OF SEQ ID NOS: 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Ruprecht, Ruth M.
APPLICANT: Shisong, Jiang
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING
TITLE OF INVENTION: A CYTOTOXIC T LYMPHOCYTE IMMUNE RESPONS
FILE REFERENCE: DFN-043CN
CURRENT APPLICATION NUMBER: US/11/022,562
CURRENT FILING DATE: 2004-12-22
CURRENT FILING DATE: 2004-12-22
                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: PCT/US03/20322
PRIOR FILING DATE: 2003-06-27
PRIOR APPLICATION NUMBER: 60/392718
PRIOR FILING DATE: 2002-06-27
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mes 5; Conserv
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                                                                                               213 IVÝQSKFL 220
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RIMFDRRF 224
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71.4%;
                                                                                                                                                                                               59.6%;
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Pred. No. 18;
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Pred. No. 41;
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Sequence 3174, Application US/10793626

; Publication No. US20050255478A1

; GENERAL IMFORMATION:

APPLICANT: KIMMERLY, WILLIAM JOHN

; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS

FILE REFERENCE: PUJ480US

; CURRENT APPLICATION NUMBER: US/10/793,626

; CURRENT FILING DATE: 2004-03-04

; PRIOR APPLICATION NUMBER: 60/164,258

PRIOR FILING DATE: 1999-11-09

; NUMBER OF SEQ ID NOS: 4472

; SOFTMARE: Patentin Ver. 2:1

; SOFTMARE: Patentin Ver. 2:1

; EQ ID NO 3174

LENGTH: 429

; TYPE: PRT

; ORGANISM: Artificial Sequence

FEATURE:
    COURTENT TON. Description of Artificial Sequence graphers.
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US-10-793-626-3174
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PRIOR FILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 2774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Publication No. US20050255478A1
GENERAL INFORMATION:
APPLICANT: KIMMERLY, WILLIAM JOHN
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REFERENCE: PU3480US
CURRENT APPLICATION NUMBER: US/10/793,626
CURRENT FILING DATE: 2004-03-04
                  Sequence 915, Application US/10821234

Publication No. US20050255114A1

GENERAL INFORMATION:

APPLICANT: Labat, Ivan

APPLICANT: Stache-Crain, Birgit

APPLICANT: Andarmani, Susan

APPLICANT: Tang, Y. Tom

APPLICANT: Tang, Y. Tom
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CURRENT APPLICATION NUMBER: US/10/821,234
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TYPE: PRT
ORGANISM: Artificial Sequence
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Local Similarity 83.3%;
es 5; Conservative
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37.5%;
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Pred. No. 44;
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41;
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US-10-821-234-1581
, Sequence 1581, Application US/10821234
; Publication No. US20050255114A1
, GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
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CURRENT FILING DATE: 2005-02-10
PRIOR APPLICATION NUMBER: 60/543,296
PRIOR FILING DATE: 2004-02-11
PRIOR FILING DATE: 2004-02-11
PRIOR APPLICATION NUMBER: 60/580,347
PRIOR APPLICATION NUMBER: 10/293,418
PRIOR FILING DATE: 2002-11-14
PRIOR FILING DATE: 2002-11-14
PRIOR FILING DATE: 2002-11-16
PRIOR FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: 60/340,817
PRIOR APPLICATION NUMBER: 60/340,817
PRIOR APPLICATION NUMBER: 60/340,817
PRIOR APPLICATION NUMBER: 09/880,748
PRIOR APPLICATION NUMBER: 09/880,748
PRIOR APPLICATION NUMBER: 09/80,748
PRIOR APPLICATION NUMBER: 09/293,499
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILLING DATE: 2001-05-25
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; ORGANISM: Homo sapiens
US-10-821-234-915
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PRIOR APPLICATION NUMBER: US 60/462,047
PRIOR FILING DATE: 2003-04-07
NUMBER OF SEQ ID NOS: 1704
SOFTWARE: pt SEQ_genes Version 1.0
SEQ_ID_NO 915
                                                                                                                                                                                                                                                                         Best Local Similarity
Matches 5; Conserv
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GENERAL INFORMATION:
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PRIOR FILING DATE: 2000-10-17
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 3247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILE REFERENCE: PF523P3
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TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 251
TYPE: PRT
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nes 6; Conservarion
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FILING DATE: 2001-03-21
APPLICATION NUMBER: 60/276,248
FILING DATE: 2001-03-16
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. US20050255532A1
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83.3%;
                                                                                                                                                                                                                                                                         Score 27; DB Pred. No. 41; 0; Mismatches
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Pred. No. 49;
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APPLICANT: WOOD, WILLIAM
APPLICANT: Zhang, Zemin
APPLICANT: Yood, WILLIAM
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C128
CURRENT APPLICATION NUMBER: U$/10/131,826A
CURRENT APPLICATION NUMBER: U$/10/131,826A
CURRENT FILING DATE: 2002-04-24
PRIOR APPLICATION NUMBER: 60/056974
PRIOR APPLICATION NUMBER: 60/056974
PRIOR APPLICATION NUMBER: 60/05913
PRIOR APPLICATION NUMBER: 60/05913
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059115
PRIOR APPLICATION NUMBER: 60/059117
PRIOR APPLICATION NUMBER: 60/059117
PRIOR APPLICATION NUMBER: 60/059122
PRIOR APPLICATION NUMBER: 60/059122
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059124
PRIOR APPLICATION NUMBER: 60/059184
PRIOR APPLICATION NUMBER: 60/059
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US-10-131-826A-452
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PRIOR FILING DATE: 2003-04-07
NUMBER OF SEQ ID NOS: 1704
SOFTWARE: pt SEQ_genes Version 1.0
SEQ ID NO 1581
LENGTH: 402
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TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
FILE REFERENCE: 821A
CURRENT APPLICATION NUMBER: US/10/821,234
CURRENT FILING DATE: 2004-04-07
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APPLICATION NUMBER: 60/059588 FILING DATE: 1997-09-19
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Wood, William
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Godowski, Paul J.
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Andarmani, Sus
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APPLICANT: Labat, Ivan
APPLICANT: Stache-Crain, Birgit
APPLICANT: Andarmani, Susan
APPLICANT: Tang, Y. Tom
APPLICANT: Tang, Y. Tom
ITITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
FILE REFERENCE: 821A
CURRENT APPLICATION NUMBER: US/10/821,234
CURRENT FILING DATE: 2004-04-07
PRIOR APPLICATION NUMBER: US 60/462,047
PRIOR APPLICATION NUMBER: US 60/462,047
PRIOR FILING DATE: 2003-04-07
NUMBER OF SEG ID NOS: 1704
SOFTWARE: pt SEQ_genes Version 1.0
SEQ ID NO 1083
LENGTH: 1150
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NUMBER OF SEQ ID NOS: 550
SEQ ID NO 452
LENGTH: 477
TYPE: PRT
ORGANISM: Homo Sapien
US-10-131-826A-452
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; ORGANISM: Homo sapiens
; FEATURE;
; NAME/KEY: misc_feature
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; OTHER INFORMATION: Xaa = any amino acid or nothing
US-10-821-234-1083
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Search completed: November 29, 2005, 23:04:38 Job time : 2.75 secs
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ALIGNMENTS

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RESULT 1
ABP83755
   Human; 121P2A3; cytostatic; immunostimulant; vaccine; SSH; humoral immune response; cellular immune response; suppression subtractive hybridisation; HLA; human leukocyte antigen.
The invention relates to a novel composition comprising a substance that modulates the status of a protein, 121P2A3. The composition of the invention has cytostatic and immunostimulant activity, and is useful as a vaccine. The 121P2A3 proteins and polynucleotides are useful for eliciting humoral or cellular immune response. The polynucleotides are useful for characterising cytogenetic abnormalities of this chromosomal locus, as tools that can be used to delineate cytogenetic abnormalities
                                                                                                                                                             New composition comprising a substance that modulates the status of 121P2A3 polypeptides, useful for eliciting humoral or cellular immune responses or in assessing the status of 121P2A3 gene products in normal
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Afar DEH, Saffran
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25-APR-2001; 2001US-0286630P.
22-JUN-2001; 2001US-0300373P.
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                                                                                                                   Claim 13; Page 130; 362pp; English.
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                                                                                                                                                 versus cancerous tissues.
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n K, M
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W, Jakobovi
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RESULT 2
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invention has cytostatic and immunostimulant activity, and is useful as a vaccine. The 12192A3 proteins and polynucleotides are useful for eliciting humoral or cellular immune response. The polynucleotides are useful for characterising cytogenetic abnormalities of this chromosomal locus, as tools that can be used to delineate cytogenetic abnormalities in the chromosomal region that encodes 12192A3 that may contribute to malignant phenotype, and in assessing the status of 12192A3 gene products in normal versus cancerous tissues. The proteins are useful for generating and characterising domain-specific antibodies, for identifying
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New composition comprising a substance that modulates the status of 121P2A3 polypeptides, useful for eliciting humoral or cellular immune responses or in assessing the status of 121P2A3 gene products in norms
                                                                                                                                                                                                                                                                                                       The invention relates to a novel composition comprising a substance that modulates the status of a protein, 121P2A3. The composition of the
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Afar DEH, Saffran
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25-APR-2001; 2001US-0286630P
22-JUN-2001; 2001US-0300373P
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n D, Morrison
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on K, Morr
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                     The invention relates to a novel composition comprising a substance that modulates the status of a protein, 121223. The composition of the invention has cytostatic and immunostimulant activity, and is useful as a vaccine. The 121223 proteins and polynucleotides are useful for eliciting humoral or cellular immune response. The polynucleotides are useful for composition that can be used to delineate cytogenetic abnormalities in the chromosomal region that encodes 12123 that may contribute to malignant phenotype, and in assessing the status of 121223 gene products in normal versus cancerous tissues. The proteins are useful for generating and characterising domain-specific antibodies, for identifying agents or cellular factors that bind to 121223 or a particular structure domain, and in various therapeutic and diagnostic contexts, including cancer vaccines. The antibodies or cells reactive with the product are
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New composition comprising a substance that modulates the status 121P2A3 polypeptides, useful for eliciting humoral or cellular in responses or in assessing the status of 121P2A3 gene products in versus cancerous tissues.
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                                                                                  The invention relates to a novel composition comprising a substance that cc modulates the status of a protein, 121P2A3. The composition of the cinvention has cytostatic and immunostimulant activity, and is useful as a cytostatic and immunostimulant activity, and is useful as a cytostatic and immunostimulant activity, and is useful as a cytostatic proteins and polynucleotides are useful for capture or cellular immune response. The polynucleotides are cytostatic abnormalities of this chromosomal control cytostatic abnormalities of the chromosomal region that encodes 121P2A3 that may contribute to complete the chromosomal region that encodes 121P2A3 that may contribute to complete the chromosomal region that encodes 121P2A3 that may contribute to complete the chromosomal region that encodes 121P2A3 that may contribute to complete the chromosomal region that encodes 121P2A3 that may contribute to complete the chromosomal region that encodes 121P2A3 that may contribute to contribute for contrating and characterising domain-specific antibodies, for identifying agents or cellular factors that bind to 121P2A3 or a particular structure complete contexts, including context vaccines. The antibodies or T cells reactive with the product are useful in passive or active immunisation, and in imaging methodologies of for the management of cancer. The sequences shown in ABB83646 - ABB95595
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25-APR-2001; 2001US-0286630P.
22-JUN-2001; 2001US-0300373P.
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                                                                 peptides from the 121P2A3 variants of the invention
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Pred. No. 2e+06;
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n K, Morrison RK, Ge
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13 variants of the invention
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W, Jakobovi
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RESULT 5
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                                                The invention relates to a novel composition comprising a substance that CC modulates the status of a protein, 121P2A3. The composition of the CC invention has cytostatic and immunostimulant activity, and is useful as a CC vaccine. The 121P2A3 proteins and polymucleotides are useful for celiciting humoral or cellular immune response. The polymucleotides are CC useful for characterising cytogenetic abnormalities of this chromosomal locus, as tools that can be used to delineate cytogenetic abnormalities in hormal versus cancerous tissues. The proteins are useful for CC malignant phenotype, and in assessing the status of 121P2A3 gene products in normal versus cancerous tissues. The proteins are useful for CC agents or cellular factors that bind to 121P2A3 or a particular structure domain, and in various therapeutic and diagnostic contexts, including CC cancer vaccines. The antibodies or T cells reactive with the product are useful in passive or active immunisation, and in imaging methodologies for the management of cancer. The sequences shown in ABP83646 - ABP95595
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25-APR-2001; 2001US-0286630P.
22-JUN-2001; 2001US-0300373P.
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Afar DEH, Saffran
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n D, Morrison K, N
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Pred. No. 2e+0
0; Mismatches
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2e+06;
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cison RK,
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Ge <sup>1</sup>
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Conservative

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Score 11; DB 6; Pred. No. 2e+06; 0; Mismatches

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                                                                                                                     Query Match
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Matches 2
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25-APR-2001; 2001US-0286630P
22-JUN-2001; 2001US-0300373P
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Afar DEH, Saffran
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               versus cancerous tissues.
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YSTTAL
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                                                                                                                        Conservative
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In D, Morrison
                                                                                                                                                   57.9%;
                                                                                                                  Score 11; DB 6;
Pred. No. 2e+06;
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RESULT 8

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                                                            Query Match
Best Local S
Matches 2
                                                                                                                           Sequence 9 AA;
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25-APR-2001; 2001US-0286630P
22-JUN-2001; 2001US-0300373P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    versus cancerous tissues.
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33.3%;
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                                                                             Score 11;
Pred. No.
                                                             Mismatches
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                                                                             DB 6;
2e+06;
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rison RK, Ge
                                                             4.
                                                                                          Length
                                                             Indels
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RESULT 9
ABP87077
ID ABP8
XX
AC ABP8
XX
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Best Local S
Matches 2
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25-APR-2001; 2001US-0286630P.
22-JUN-2001; 2001US-0300373P.
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                                                                                                                                                                                                                                                                        Sequence 9 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 13; Page 186; 362pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New composition comprising a substance that modulates the status of 121P2A3 polypeptides, useful for eliciting humoral or cellular immune responses or in assessing the status of 121P2A3 gene products in normal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    versus cancerous tissues.
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                   ABP87077;
                                                      ABP87077 standard; peptide; 9 AA
                                                                                                                                                                                                       Local Similarity 33...
nes 2; Conservative
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nn D, Morrison K, Mor
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33.3%;
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                                                                                                                                                                                                                          Score 11; DB 6;
Pred. No. 2e+06;
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Morrison RK, Ge
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RESULT 10
ABP88907
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SEXEXEXE
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Best Local Similarity
Matches 2; Conser
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25-APR-2001;
22-JUN-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New composition comprising a substance that modulates the status of 121P2A3 polypeptides, useful for eliciting humoral or cellular immune responses or in assessing the status of 121P2A3 gene products in norm
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Afar DEH, Saffran
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 13; Page 186; 362pp; English.
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                                                                                                                                                                                                                                                                                                                   Sequence 9
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                HLA protein
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                                                 28-MAR-2003
                                                                              ABP88907;
                                                                                                             ABP88907 standard; peptide;
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                                                                                                                                                                                                                                                                                                                      AA;
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; 2001US-0286630P.
; 2001US-0300373P.
                121P2A3 peptide #5262
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                                                (first entry)
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33.3%;
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Morrison K, Morrison RK, Ge
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Pred. No.
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2e+06;
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W, Jakobovi
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RESULT 11
ABP89307
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                                                                                                                                                                                                                                                                                                                                                                        Query Match
            Human; 121P2A3; cytostatic; immunostimulant; vaccine; SSH; humoral immune response; cellular immune response; suppression subtractive hybridisation; HLA; human leukocyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; 121P2A3; cytostatic; immunostimulant; vaccine; SSH; humoral immune response; cellular immune response; suppression subtractive hybridisation; HLA; human leukocyte antigen.
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Afar DEH, Saffran
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25-APR-2001; 2001US-0286630P.
22-JUN-2001; 2001US-0300373P.
                                                                                                                  28-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 9 AA;
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                                                                                                                                                    ABP89307
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n D, Morrison
                                                                               peptide
                                                                                                                  entry)
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                                                                                 #5662
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Pred. No. 2e+06;
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on K, Morri
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Morrison RK, Ge
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W, Jakobovi
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RESULT 12
ABP84056
ID ABP84
XX ABP84
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XX ABP84
XX ABP84
XX Human
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XW Human
XW Suppx
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Best Local :
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25-APR-2001; 2001US-0286630P
22-JUN-2001; 2001US-0300373P
                   WO200283068-A2
                                                  Homo sapiens.
                                                                               suppression
                                                                                 Human; 121P2A3; cytostatic; immunostimulant; vaccine; SSH; humoral immune response; cellular immune response; suppression subtractive hybridisation; HLA; human leukocyt
                                                                                                                                                   HLA protein 121P2A3 peptide
                                                                                                                                                                                      28-MAR-2003
                                                                                                                                                                                                                                                    ABP84056 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           versus cancerous tissues.
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2; Conserv
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33.3%;
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Pred. No.
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on K, Morr
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                                                                                     leukocyte
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W, Jakobovi
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RESULT 13
ABP84643
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Best Local S
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                                                                                                                                Human; 121P2A3; cytostatic; immunostimulant; vaccine; SSH; humoral immune response; cellular immune response; suppression subtractive hybridisation; HLA; human leukocyte antigen.
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              09-APR-2002; 2002WO-US011359
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RESULT 14
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Afar DEH, Saffran D,
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              10-APR-2001; 2001US-0282739P.
25-APR-2001; 2001US-0286630P.
22-JUN-2001; 2001US-0300373P.
                                                                                                                                                                                                                  Human; 121P2A3; cytostatic; immunostimulant; vaccine; SSH; humoral immune response; cellular immune response; suppression subtractive hybridisation; HLA; human leukocyte antigen.
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The invention relates to a novel composition comprising a substance that CC modulates the status of a protein, 121P2A3. The composition of the CC invention has cytostatic and immunostimulant activity, and is useful as a CC vaccine. The 121P2A3 proteins and polynucleotides are useful for CC eliciting humoral or cellular immune response. The polynucleotides are CC useful for characterising cytogenetic abnormalities of this chromosomal CC locus, as tools that can be used to delineate cytogenetic abnormalities CC in the chromosomal region that encodes 121P2A3 that may contribute to CC malignant phenotype, and in assessing the status of 121P2A3 gene products CC in normal versus cancerous tissues. The proteins are useful for CC generating and characterising domain-specific antibodies, for identifying agents or cellular factors that bind to 121P2A3 or a particular structure CC domain, and in various therapeutic and diagnostic contexts, including CC cancer vaccines. The antibodies or T cells reactive with the product are CC useful in passive or active immunisation, and in imaging methodologies CC for the management of cancer. The sequences shown in ABP83646 - ABP95595 CC represent peptides from the 121P2A3 variants of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New composition comprising a substance that modulates the status of 121P2A3 polypeptides, useful for eliciting humoral or cellular immune responses or in assessing the status of 121P2A3 gene products in normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 13; Page 182; 362pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    versus cancerous tissues.
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Search completed: November 29, Job time: 96.4546 secs 밁 Ś Matches Similarity 2; Conserv N 4 YXXXXL YSTTTL Conservative 2005, 22:52:19 Score 11; DB Pred. No. 2e+0 0; Mismatches 0

Query Match Best Local 9

57.9%;

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Copyright (c) 1993 - 2005 Compugen Ltd.
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Score 11; DB 2; Pred. No. 1.8e+02; 0; Mismatches 4

4; Indels Length 38;

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0;

57.9%; 33.3%;

RESULT 2 D82306 hypothetical protein VC0584 [imported] - Vibrio cholerae (sc;Species: Vibrio cholerae C;Species: Vibrio cholerae C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_ch C;Accession: D82306 R;Heidelberg, J.F; Eisen, J.A.; Nelson, W.C.; Clayton, R.A. chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qi. l, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M. Nature 406, 477-483, 2000 A;Title: DNA Sequence of both chromosomes of the cholera pa A;Reference number: A82035; MUID:20406833; PMID:10952301 A;Accession: D82306 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-38 <hei> A;Cross-references: UNIPROT:Q9KUD8; UNIPARC:UPI00000C2D29; A;Experimental source: serogroup O1; strain N16961; biotype C;Genetics: A;Gene: VCOS84 A;Map position: 1</hei>	RESULT 1 PH1314 Ig heavy chain DJ region (clone C200-98) - human (fragm C; Species: Homo sapiens (man) C; Species: Homo sapiens (man) C; Species: Homo sapiens (man) C; Accession: PH1314 R; Wasserman, R; Galili, N: Iro, Y:; Reichard, B.A.; S J. Exp. Med. 176, 1577-1581, 1992 J. File: Predominance of fetal type DJH joining in youn A; Ticle: Predominance of Fetal type DJH joining in youn A; Reference number: PH1302; MUID:93094761; PMID:1460419 A; Accession: PH1314 A; Molecule type: DNA A; Residues: 1-15 < WABS A; Cross-references: UNIPARC:UPI000017C235 A; Cross-references: UNIPARC:UPI000017C235 C; Keywords: heterotetramer; immunoglobulin Query Match Best Local Similarity 33.3%; Pred. No. 89; Matches 2; Conservative 0; Mismatches 4; Oy 4 YXXXXL 9 Db 2 YSSSL 7	30 11 57.9 94 2 A01955 31 11 57.9 95 2 S45324 32 11 57.9 95 2 S69888 32 11 57.9 95 2 PH008G3 34 11 57.9 98 2 PH106C2 35 11 57.9 101 2 C28840 37 11 57.9 101 2 B3726C2 38 11 57.9 104 2 F87731 40 11 57.9 106 2 PL02G0 41 11 57.9 106 2 PL02G0 42 11 57.9 106 2 PL02G0 43 11 57.9 106 2 PL02G0 44 11 57.9 107 2 S3626C2 45 11 57.9 107 2 S3626C2 46 11 57.9 107 2 S3626C2 47 11 57.9 107 2 S3626C2
<pre>cholerae (strain N16961 serogroup O1) 00 #text_change 09-Jul-2004 llayton, R.A.; Gwinn, M.L.; Dodson, R.J. lass, S.; Qin, H.; Dragoi, I.; Sellers, c.M. cholera pathogen Vibrio cholerae. 10952301 10952301 61; biotype El Tor</pre>	(fragment) #text_change 07-May-1999 .A.; Shane, S.; Rovera, G. n young children with B precursor lymple 460419 ; Length 15; 4; Indels 0; Gaps 0;	Ig kappa-B5 chain Ig kappa chain V r Ig kappa chain V r Ig kappa chain V r Ig light chain V r Ig light chain V r Ig kappa chain V r Ig kappa chain V r Ig kappa chain V r Ig kappa chain V r Ig kappa chain V r Ig kappa chain V r Ig kappa chain V r Ig kappa chain V r Ig kappa chain V r Ig kappa chain V r Ig kappa chain V r Ig kappa chain V r Ig kappa chain V r Ig kappa chain V r Ig lambda chain V Ig lambda chain V Ig lambda chain V

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A;Molecule type: DNA
A;Residues: 1-46 <STO>
A;Cross-references: UNIF
A;Experimental source: 8
A;Accession: B85717
14K hypothetical thioredoxin-related cycX 3' region protein - Bradyrhizobiu C;Species: Bradyrhizobium japonicum C;Date: 30-Dec-1991 #sequence_revision 30-Dec-1991 #text_change 09-Jul-2004
                                                                                                                     RESULT 5
E39741
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JT0521
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A;NOte: the sequence shown here is one of eight productive V-D-J
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-49/Domain: V region <VRE>
F;50-54/Domain: J region <JRE>
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A; Residues: 1-54 < ANK>
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J. Exp. Med. 169, 2109-2119, 1989
A;Title: Clonal diversity in the B cell repertoire of patients with X-linked agammaglobu
A;Reference number: JT0511; MUID:89279157; PMID:2786547
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A;Experimental source: strain O157:H7, substrain EDL933
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;Species: Homo sapiens (man)
;Date: 23-Oct-1992 #sequence_revision 23-Oct-1992 #text_change 09-May-1997
;Accession: JT0521
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Pred. No. 2e+02;
0; Mismatches
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2.3e+02;
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C;Accession: E39741
R;Ramseier, T.M.; Winteler, H.V.; Hennecke, H.
J. Biol. Chem. 266, 7793-7803, 1991
A;Title: Discovery and sequence analysis of bacterial genes involved:
A;Reference number: A39741; MUID:91210304; PMID:1850420
A;Accession: E39741
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-61 <RAM>
A;Cross-references: UNIPROT:P30959; UNIPARC:UPI000005E784; GB:M60874;
                                                                                                                                                                                                                                RESULT 7
F90970
A;Reference number: A99629;
A;Accession: F90970
A;Status: preliminary
                             DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7
A:Reference number: A99629; MUID:21156231; PMID:11258796
                                                                                                  C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change C;Accession: F90970
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Gene: 3
C;Superfamily: phage lambda head-to-tail joining C;Keywords: head protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Smith, M.P.; Feiss, M.
J. Bacteriol. 175, 2393-2399, 1993
A;Title: Sites and gene products involved in lambdoid phage DNA
A;Title: Sites and gene products involved in lambdoid phage DNA
A;Title: Sites and gene products involved in lambdoid phage DNA
A;Title: Sites and gene products involved in lambdoid phage DNA
A;Accession: (49849)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gene 126, 1-7, 1993
A;Title: Sequence analysis of the phage 21
A;Reference number: JN0537; MUID:93231520;
A;Accession: JN0537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Date: 17-Feb-1994 #sequence_revision C; Accession: JN0537; C49849
                                                                                                                                                                                       probable head completion protein [imported] -
C;Species: Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: UNIPARC:UPI0000174BC3
A;Note: sequence extracted from NCBI backbone (NCBIN:129221, NCBIP:129224)
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C;Date: 17-Feb-19
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A; Residues: 1-27 <SM2>
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A;Residues: 1-68 <SMI>
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Shinagawa,
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A;Residues: 1-68 <HAY>
A;Cross-references: UNIPROT:Q8XC12; UNIPARC:UPI0000D0524; GB:BA000007; PIDN:BAB36157.1
A;Experimental source: strain O157:H7, substrain RIMD 0509952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Accession: A03878
R;NIles, E.G.; Condit, R.C.; Caro, P.; Davidson, K.; Matusick, L.; Seto, J.
Virology 153, 96-112, 1986
A;Title: Nucleotide sequence and genetic map of the 16-kb vaccinia virus HindIII D fragm
A;Reference number: A01146; MUID:86291159; PMID:3739227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein D-69 - vaccinia virus (strain WR)
C;Species: vaccinia virus
C;Date: 04-Dec-1986 #sequence_revision 04-Dec-1986 #text_change 09-Jul-2004
C;Accession: A03878
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submitted to GenBank, June 1990
A;Reference number: A33172
A;Accession: F42316
Ig kappa chain V region - human (fragment)
C;Specites: Homo sapiens (man)
C;Date: 20-Feb-1995 #sequence_revision 25-Oct-1996 #text_change 23-Jul-1999
C;Accession: S34082; S21526
R;Wagner, S.D.; Luzzatto, L.
                                                                                           RESULT 10
S21526
                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-69 <JOH>
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A;Note: host Homo sapiens (man)
C;Date: 09-Nov-1990 #sequence_revision
C;Accession: F42516
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A; Residues: 1-69 <NIL>
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Pred. No. 2.8e+02;
0; Mismatches 4
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Pred. No. 2.7e+02;
D; Mismatches 4
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Pred. No. 2.8e+0
0; Mismatches
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A;Cross-references: UNIPARC:UPI000011604F; EMBL:X66042; NID:g33318; C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin
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A;Molecule type: DNA
A;Residues: 1-71 <WA2>
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A;Title: V-kappa gene segments rearranged in chronic lymphocytic leukemia are distributë
A;Reference number: S34076; MUID:93170387; PMID:8436174
A;Accession: S34082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein a183L - Chlorella virus PBCV-1
C;Species: Chlorella virus PBCV-1
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
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R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K. Lancet 357, 1225-1240, 2001

A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aur A;Reference number: A89758; MUID:21311952; PMID:11418146
                                                                                                                                                                                                                                                                                                                                                          hypothetical protein [imported] - Staphylococcus aureus (strain N315)
C;Species: Staphylococcus aureus
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
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A; Residues: 1-76 < GRA>
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A; Accession: T17673
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A;Experimental source: specific host
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                                                                                                                                              A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-81 <KUR>
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                                                                                                            A;Cross-references: UNIPROT:Q99V57;
A;Experimental source: strain N315
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Pred. No.
                     Score 11; I
Pred. No. 3
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c Chlorella strain NC64A
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RESULT 15
316840
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C;Accession: S16840
R;Blaison, G.; Kuntz, J.L.; Pasquali, J.L.
Bur. J. Immunol. 21, 1221-1227, 1991
A;Title: Molecular analysis of V(Rappa);II variable regions of polyclonal rheumatoid A;Reference number: S16823; MUID:91243737; PMID:1903706
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Wagner, S.D.; Luzzatto, L. Eur. J. Immunol. 23, 391-397, 1993
Eur. J. Immunol. 23, 391-397, 1993
A;Title: V-kappa gene segments rearranged in chronic lymphocytic leukemia are distribute
A;Reference number: S34076; MUID:93170387; PMID:8436174
A;Accession: S34086
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C;Species: Homo Bapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
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A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: F87306
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A; Residues: 1-86 < WAG>
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C;Superfamily: conserved hypothetical protein HI1000
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A;Molecule type: DNA
A;Residues: 1-84 <STO>
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A;Molecule type: mRNA
A;Residues: 1-86 <BLA>
A;Residues: 1-86 <BLA>
A;Cross-references: UNIPROT:Q96SA9; UNIPARC:UPI0000176DA5; EMBL:X54838
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
C;Keywords: heterotetramer; immunoglobulin
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Pred. No. 3.2e+02;
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Search completed: November 29, 2005, 23:02:35 Job time: 17.6818 secs

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Title:
Perfect score:
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Gapop 10.0 , Gapext 0.5
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1: uniprot_sprot:*
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      GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.
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QSKUDB_VIBCH
QSKC12_EKULA
QSAFM3_SHIFL
QSAFM3_SHIFL
QSAFM3_SHIFL
QSAFM3_SHIFL
QSAFM3_PVIRU
QSGABB_9VIRU
QSGABB_SVIRU
QSGABB_SHFIL
VG03_BFP21
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VG03_BFP21
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Q77ST4_CAMPS
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Q6CB16_YARLI
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Q7acv9
Q5pan6
Q8fih6
P20552
P04304
Q9ams1
Q7mrv7
Q7mrv7
Q7mrv1
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    1 bradyrhizob
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4 camelpox vi
0 oryza sativ
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STRAIN=E1 Tor N16961 / Serotype 01;

STRAIN=E20406833; PubMed=10952301; DDI=10.1038/35020000; MEDLINE=20406833; PubMed=10952301; DDI=10.1038/350200000; MEDLINE=20406833; PubMed=10952301; DDI=10.1038/35020000; MEDLINE=2040683; PubMed=10952301; DDI=10.1038/35020000;  PubMed=10952301; DDI=10.1038/35020000; PubMed=10952301; DDI=10.1038/350200000; PubMed=10952301; DDI=10.1038/350200000; PubMed=
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Science 307:82-86(2005).

-I- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is preliminary data.
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Bacteria; Proteobacteria;
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MEDLINE=21074935; PubMed=11206551; DOI=10.1038/35054089;
Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
Welch R.A., Blattner F.R.;
"Genome semmence of ---
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OrderedLocusNamese=z2132, z2363;

Escherichia coli ordered.
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01-MAR-2002 (TrEMBLrel. 20, Last
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Mekalanos J.J., Venter J.C., Frase
"DNA sequence of both chromosomes
                                                                                                                                                                                                                                                                 PIR; E85743; E85743.
PIR; F90970; F90970.
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fam; PF02831; gpW; 1.
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4133 MW; BA86FA65823A8899
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A Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla B.,
A Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla B.,
A Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
A Barnay S., Blanchin S., Beckerich J.-M., Beyne E., Bleykasten C.,
A Boisrame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A.,
A Bespons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
A Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
A Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
A Nicaud J.-M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
A Pellenz S., Potier S., Richard G.-F., Straub M.-L., Suleau A.,
A Pellenz S., Potier S., Richard G.-F., Straub M.-L., Suleau A.,
A Seniou-Meyer M., Zivanovic Y., Bolotin-Fukuhara M., Thierry A.,
A Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
A Wincker P., Souciet J.-L.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-2001 (TrEMBLrel. 17, 01-JUN-2001 (TrEMBLrel. 17, 01-JUN-2003 (TrEMBLrel. 24,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Fungi; Aacomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
                                                                                                                                                                                      Infect. Immun. 69:3271-3285(2001).
EMBL, AF348706; AAK18546.1; -; Gen
Hypothetical protein; Plasmid.
BEQUENCE 49 AA; 5174 MW; 81FEC
                                                                                                                                                                                                                                                                                            NUCLEOTIDE SEQUENCE.
MEDLINE=21189246; PubMed=11292750;
DOI=10.1128/IAI.69.5.3271-3285.2001;
Venkatesan M.M., Goldberg M.B., Rose D.J.,
Blattner F.R.;
Blattner F.R.;
"Complete DNA sequence and analysis of the
Shigella flexneri.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Plasmid virulence plasmid pWR501.
Bacteria; Proteobacteria; Gammaproteobacteria;
Enterobacteriaceae; Shigella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Shigella flexneri.
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Q9AFM3;
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EMBL; CR382122; CAH02420.1; -;
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Pred. No. 1.9e+03
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                                                                                                                               The mitochondrial genome of the olive fly Bactrox Applets Promise From distant geographical locations.";

RI Insect Mol. Biol. 12:605-611(2003).

REMBL; AY210703; AA034658.1; -; Genomic DNA.

DR EMBL; AY210702; AA034658.1; -; Genomic DNA.

DR GO; GO:0016020; C:membrane; IEA.

DR GO; GO:0015029; C:mitochondrion; IEA.

DR GO; GO:00146283; C:proton-transporting ATP synthase R GO; GO:0016893; F:hydrogen-transporting ATP synthase R GO; GO:0046931; F:hydrogen-transporting ATP synthase R GO; GO:0046961; F:hydrogen-transporting ATP synthase R GO; GO:0016811; P:ion transport; IEA.

R GO; GO:0015992; P:proton transporting ATP synthase R GO; GO:0016811; P:ion transporting ATP synthase R GO; GO:0016811; P:ion transport; IEA.
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10-MAY-2005
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Wang H.-S., Lee Y.-S.;
"The genome sequence of Salmonella enterica serovar Choleraesuis, highly invasive and resistant zoonotic pathogen.";
Nucleic Acids Res. 33:1690-1698 (2005).
EMBL; AE017220; AAX68200.1; -; Genomic_DNA.
Complete proteome; Hypothetical protein.
Complete S1 AA; 5645 MW; BF41842EEDF831DB CRC64;
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Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Salmonella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence up
10-MAY-2005 (TrEMBLrel. 30, Last annotation
ATP synthase F0 subunit 8.
Bactrocera oleae (Olive fruit fly).
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OrderedLocusNames=SC4294;
                              GO; GO:0016020; C:membrane; IBA.
GO; GO:0016739; C:mitochondrion; IEA.
GO; GO:0005739; C:mitochondrion; IEA.
GO; GO:0016453; C:proton-transporting ATP synthase complex; IEA.
GO; GO:0016469; C:proton-transporting Two-sector ATPase complex; IEA.
GO; GO:0016469; F:hydrogen-transporting ATP synthase activity. rota. .;
GO; GO:001691; F:hydrogen-transporting ATPase activity, rota. .;
GO; GO:0015986; P:ATP synthesis coupled proton transport; IEA.
GO; GO:0015986; P:ion transport; IEA.
GO; GO:0015992; P:proton transport; IEA.
InterPro; IPR001421; ATPase8_mit.
Pfam; PF00895; ATP-synt_8; 1.
CF(0); Hydrogen ion transport; Ion transport; Mitochondrion;
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lli A., Dallai R., Frati F.;
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Pred. No. 2e+03;
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RESULT 10
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SEQUENCE
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01-UUL-1993 (Rel. 26, Last sequence update)
10-WAY-2005 (Rel. 47, Last annotation update)
10-WAY-2005 (Rel. 10)
Heme exporter protein D (Cytochrome c-type biogenesis protein
Name=cycX; Synonyms=ccmD; OrderedLocusNames=bsr0470;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BRAJA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Complete genomic sequence of nitrogen-fixing symbiotic bacterium Bradyrhizobium japonicum USDA110."; DNA Res. 9:189-197(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=91210304; PubMed=1850420;
Ramseler T.M., Winteler H.V., Hennecke H.;
"Discovery and sequence analysis of bacterial genes
biogenesis of c-type cytochromes.";
J. Biol. Chem. 266:7793-7803(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bradyrhizobium japonicum.
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Bradyrhizobiaceae; Bradyrhizobium.
                                                                                                                                                                                                          Complete proteome; Cytochrome c-type biogenesis; Membrane; Transmembrane; Transport.
TRANSMEM 11 31 Potential.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA Res. 9:189-197(2002).

-I- FUNCTION: Required for the export of heme to the phiogenesis of c-type cytochromes (Potential).

-I- SIMILARITY: Belongs to the ccmD/cycX/helD family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
Sasamoto S., Watanabe A., Idesawa K., Iriguchi M., Kawashin
Kahara M., Matsumoto M., Shimpo S., Tsuruoka H., Wada T., Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=USDA 110;
MEDLINE=22484998; PubMed=12597275;
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                                                                                                                                                                                                                                                                                                                                                                         EMBL; M60874; AAA26195.1; -; Genomic DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This Swiss-Prot entry is copyright. It is produced through a collaboratic between the Swiss Institute of Bioinformatics and the EMBL outstation between the Swiss Institute of Bioinformatics and the EMBL outstation to the succession of the success
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                                                                                                                                                                                                                                                                                                                           E39741; E39741.
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16
                                                                                                                                                                                                                                                                               PF04995; CcmD;
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                                                                                                                                                                                    61 AA; 6776 MW;
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                                                                                          Conservative
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33.3%;
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33.3%;
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0; Mismatches
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Pred. No.
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BC6B9852E927370A CRC64;
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                                                                                                                                   Length 61,
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RESULT 11

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Q6BXJ7_DEBHA
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ID QBVMA9;

AC QBVMA9;

DT 01-MAR-2002 (TrEMBL:el. 2)
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A Lafontaine I. de Montigny J., Marck C., Neuveglise C., Talla E.,
A Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
A Barnay S., Blanchin S., Beckerich J.-M., Beyne E., Bleykasten C.,
A Boisrame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A.,
A Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
A Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
A Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
A Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
A Kerrest A., Nicolski M., Oztas S., Ozier-Kalogeropoulos O.,
A Pellenz S., Potter S., Richard G.-F., Straub M.-L., Suleau A.,
A Pellenz S., Potter S., Richard G.-F., Straub M.-L., Suleau A.,
A Swennen D., Tekala F., Weeolowski-Louvel M., Westhof E., Wirth B.,
A Seniou-Meyer M., Zivanovic Y., Bolotin-Fukuhara M., Thierry A.,
Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
Mincker P., Souciet J.-L.,
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Rhizobiaceae; Rhizobium/Agrobacterium group; Rhizobium.
NCBI_TaxID=29449;
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EMBL; CR382134; CAG85060.1; -; Genomic_DNA.
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PubMed=15681403; DOI=10.1128/JVI.79.4.2010-2023.2005;

Teal C.T., Ting J.W., Wu M.H., Wu M.F., Guo I.C., Chang '
"Complete genome sequence of the grouper iridovirus and genomic organization with those of other iridoviruses.";

J. virol. 79:2010-2023(2005).
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Song W.J., Qin Q.W., Qiu J., Huang C.H., Wang F., Hew C.L.;
Song W.J., Qin Q.W., Qiu J., Huang C.H., Wang F., Hew C.L.;
"Functional Genomics Analysis of Singapore Grouper Iridovirus:
Complete Sequence Determination and Proteomic Analysis.";
J. Virol. 78:12576-12590(2004).
EMBL; AY521225; AAS18026.1; -; Genomic_DNA.
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25-OCT-2004 (TrEMBLrel.
Hypothetical protein.
ORFNames=ORF011L;
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Viruses; dsDNA viruses,
NCBI_TaxID=127569;
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Viruses; dsDNA viruses, no RNA
                         Chang C.-Y., Tsai C.-T.;
submitted (JUN-2004) to the
EMBL; AY666015; AAV91125.1;
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Murali S., Wu M.-F.,
Submitted (MAR-2001)
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Submitted (FEB-2005)
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Chang C.-Y., Teai C.
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Tan W.G.H., Barkman T.J., Ch
Submitted (FEB-2004) to the
EMBL; AY548484; AAT09692.1;
Hypothetical protein.
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PubMed=15165820; DOI=10.1016/j.virol.2004.02.019;
PubMed=15165820; DOI=10.1016/j.virol.2004.02.019;
Tan M.G., Barkman T.J., Gregory Chinchar V., Essani
"Comparative genomic analyses of frog virus 3, type
genus Ranavirus (family Iridoviridae).";
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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Query Match 57.9%; Score 11; DB 1; Length 11; Best Local Similarity 33.3%; Pred. No. 1.4e+03; Best Local Similarity 0; Mismatches 4; Indels 0; Gaps	US-08-540-412-123 US-08-540-412-123 US-08-540-412-123 Sequence 123, Application US/08540412 Sequence 123, Application US/08540412 Patent No. 586679 GENERAL INFORMATION: Defoc-Jones, Deborah APPLICANT: Defoc-Jones, Deborah APPLICANT: Garrky, Victor M. APPLICANT: Oliff, Allen I. APPLICANTON. HOWEL PRETIDES NUMBER OF SEQUENCES: 194 CORRESSORDENCE ADDRESS: COMPTER: NEW JERSEY COUNTRY: U.S.A. CITY: RHHAY COUNTRY: U.S.A. CITY: RHHAY COUNTRY: U.S.A. CITY: AND JERSEY COUNTRY: U.S.A. COMPUTER: READABLE FORM: MEDIUM TYPE: Allen I. COMPUTER: ARBORD ALLEN MEDIUM TYPE: ALLEN MEDIUM TYPE: ALLEN MEDIUM TYPE: ALLEN MEDIUM TYPE: ALLEN APPLICATION NUMBER: US/08/540,412 FILING DATE: FILING DATE: 11 main acids THELEPAX: (908) 594-4702 INFORMATION FOR SED ID NO: 123: SEQUENCE CHARACTERISTICS: LENGTH: 11 main acids TYPE: amin acids TYPE: main acids TYPE: MOLECULE TYPE: peptide HYPOTHETICAL: NO ANTI-SENSE: Internal	28 11 57.9 88 2 US-09-905-243-34 Sequence 34, A 29 11 57.9 91 2 US-10-330-613A-64 Sequence 64, A 30 11 57.9 92 1 US-08-273-146-45 Sequence 45, A 31 157.9 92 1 US-08-273-146-53 Sequence 45, A 32 11 57.9 93 2 US-10-330-613A-44 Sequence 54, A 33 11 57.9 95 2 US-10-349-75-54 Sequence 27, A 35 11 57.9 95 2 US-10-194-975-55 Sequence 54, A 37 11 57.9 95 2 US-10-194-975-58 Sequence 55, A 37 11 57.9 95 2 US-10-194-975-58 Sequence 55, A 39 11 57.9 95 2 US-10-194-975-61 Sequence 60, A 40 11 57.9 95 2 US-10-194-975-61 Sequence 60, A 42 11 57.9 95 2 US-10-194-975-61 Sequence 61, A 41 11 57.9 95 2 US-10-194-975-65 Sequence 62, A 42 11 57.9 95 2 US-10-194-975-65 Sequence 65, A 44 11 57.9 95 2 US-10-194-975-66 Sequence 65, A 44 11 57.9 95 2 US-10-194-975-66 Sequence 65, A 54 11 57.9 95 2 US-10-194-975-66 Sequence 66, A 54 11 57.9 95 2 US-10-194-975-66 Sequence 66, A 54 11 57.9 95 2 US-10-194-975-66 Sequence 66, A 54 11 57.9 95 2 US-10-194-975-66 Sequence 66, A 54 11 57.9 95 2 US-10-194-975-69 Sequence 67, A 54 11 57.9 95 2 US-10-194-975-6
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; Patent No. 6130204
; GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: DeFeo-Jones, Deborah
APPLICANT: Feng, Dong-Mei
APPLICANT: Garsky, Victor M.
APPLICANT: Jones, Raymond E.
APPLICANT: Oliff, Allen I.
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US-08-540-412-191
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Best Local Similarity
Matches 2; Conserval
                                                                                                                                                                                          Sequence 123, Application US/09051342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 191,
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APPLICANT: Defeo-
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/540,412
FILING DATE:
CLASSIFICATION: 530
                               APPLICANT: Oliff, Allen I.
TITLE OF INVENTION: NOVEL PEPTIDES
NUMBER OF SEQUENCES: 194
                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Muthard, David A.
REGISTRATION NUMBER: 35,297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                CORRESPONDENCE ADDRESS:
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TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: UZIP: 07065
ADDRESSEE:
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5866679
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                                                                                                                                                                                                                                                                                                                                                   Conservative
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DAVID A. MUTHARD
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                                                                                                                                                                                                                                                                                                                                                                  Score 11; DB 1;
Pred. No. 1.4e+03;
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; HYPOTHETICAL: NO; ANTI-SENSE: NO; FRAGMENT TYPE: : US-09-051-342-123
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US-09-051-342-191
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Matches
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Best Local (
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
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CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Muthard, David A.
REGISTRATION NUMBER: 35,297
REFERENCE/DOCKET NUMBER: 1925
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
APPLICANT:
                                                                          COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/051,342
        FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Muthard, David A.
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MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/051,342
                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: NOVEL PEPTIDES NUMBER OF SEQUENCES: 194
                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                            STATE: NEW JERSEY COUNTRY: U.S.A. ZIP: 07065
                                                                                                                                                                                                                                                   CITY: RAHWAY
                                                                                                                                                                                                                                                                 STREET:
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REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                 ADDRESSEE: DAVID A. MUTHARD
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TYPE: amino acid
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Similarity 33.3%;
2; Conservative
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Y: U.S.A.
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                                                                                                                                                                                                                                                              126 E. Lincoln Avenue, P.O. BOX 2000
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Query Match
Best Local Similarity
"---hes 2; Conserve
                                                                              US-08-468-161-123
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Patent No. 6143864
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SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                      CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Muthard, David A.
REGISTRATION UNMBER: 35,297
REFERENCE/DOCKET NUMBER: 1925
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908)594-3903
                                                                                                                                                                                                                       TELEFAX: (908)594-4720
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                              MOLECULE TYPE: |
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (908)594-3903
                                                                                                                                                   LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Oliff, Allen I.
TITLE OF INVENTION: NOVEL PEPTIDES
NUMBER OF SEQUENCES: 146
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
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STRANDEDNESS: sir
TOPOLOGY: linear
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COUNTRY: U.S.A.
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               Conservative
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                                                                                                                        NO peptide
                                                                                               internal
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33.3%;
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Pred. No. 1.4e+03;
0; Mismatches 4
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               Score 11; DB 2; Length 11; Pred. No. 1.4e+03; 0; Mismatches 4; Indels
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FEATURE:
OTHER INFORMATION: completely synthetic amino acid sequence
US-09-051-759-123
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US-09-051-759-123
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; OTHER INFORMATION; completely synthetic amino acid sequence US-09-051-759-191
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SEQ ID NO 123
LENGTH: 11
TYPE: PRT
                                                                            SOFTWARE: FA
SEQ ID NO 191
LENGTH: 11
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 191, Application US/09051759 Patent No. 6177404
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Matches 2; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
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PRIOR APPLICATION NUMBER: 60/005,664
PRIOR PILING DATE: 1995-10-18
PRIOR APPLICATION NUMBER: PCT/US96/16490
PRIOR FILING DATE: 1996-10-15
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APPLICANT:
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Scolnick, Edward M.
TITLE OF INVENTION: CONJUGATES USEFUL IN THE TREATMENT OF
TITLE OF INVENTION: BENIGN PROSTATIC HYPERPLASIA
                                                                                                                                                                                                                                                                                            APPLICANT: Garsky, Victor M.
APPLICANT: Jones, Raymond E.
APPLICANT: Oliff, Allen I.
APPLICANT: Scolnick, Edward M.
TITLE OF INVENTION: CONJUGATES USEFUL IN THE TREATMENT
TITLE OF INVENTION: BENIGN PROSTATIC HYPERPLASIA
FILE REFERENCE: 19560P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/051,759
CURRENT FILING DATE: 1998-08-03
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                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/051,759
CURRENT FILING DATE: 1998-08-03
FRIOR APPLICATION NUMBER: 60/005,664
PRIOR FILING DATE: 1995-10-18
PRIOR APPLICATION NUMBER: PCT/US96/16490
PRIOR FILING DATE: 1996-10-15
PRIOR FILING DATE: 1996-10-15
PRIOR OF SEQ ID NOS: 194
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                                       ORGANISM: Artificial Sequence FEATURE:
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DeFeo-Jones, Debora
Garsky, Victor M.
Jones, Raymond E.
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                                                                                                                                       FastSEQ for Windows Version 4.0
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Pred. No.
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Query Match
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Best Local Similarity 3
                                     RESULT 9
5219837-5
;Patent No. 5219837
; APPLICANT: COHEN, JEFFREY A.;GREENE, MARK I.;WILLIAMS,
WILLIAM V.
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              OF CELLS
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INFORMATION FOR SEQ ID NO:
NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Muthard, David A.
REGISTRATION NUMBER: 35,297
REFERENCE/DOCKET NUMBER: 19:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                          TITLE OF INVENTION: METHOD OF STIMULATING MYELINATION
                                                                                                                                                                                                                                                               HYPOTHETICAL: NO ANTI-SENSE: NO FRAGMENT TYPE:
                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 146
CORRESPONDENCE ADDRESS:
ADDRESSEE: DAVID A. MUTHARD
                                                                                                                                                                                                                                                                                                        MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TTLE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: PCT/US95/08156 FILING DATE: CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 07065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: RAHWAY
STATE: NEW JERSEY
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TOPOLOGY: lir
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Pred. No. 1.4e+03;
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Pred. No. 1.4e+03;
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Query Match
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APPLICATION NUMBER: US/07/541,779
FILING DATE: 21-JUN-1990
SEQ ID NO:5:
LENGTH: 18
                                                                                                                                                                                                                                                                                                                                                 US-08-905-223-22
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Best Local S
                                                                                                                                                                                                    Sequence 22. Application US/08905223
Patent No. 6222029
GENERAL INFORMATION:
APPLICANT: Edwards, Jean-Baptiste D.
APPLICANT: Duelert, Aymeric
APPLICANT: Lacroix, Bruno
TITLE OF INVENTION: 5' ESTS FOR SECRETED PROTEINS
NUMBER OF SEQUENCES: 503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Harris, Curtis C
APPLICANT: Nagashima, Makoto
APPLICANT: Nagashima of United States as represented by the Secretary of the APPLICANT: Department of Health and Human Services
TITLE OF INVENTION: New Tumor Suppressor Gene P33ING2
FILE REFERENCE: 015280-376100US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 5, Application US/09513365A Patent No. 6790948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin Ver. 2.1
COUNTRY: USA
ZIP: 92101-3505
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC compatibl
OPERATING SYSTEM: Win95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/513,365A CURRENT FILING DATE: 2000-02-25
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TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: Description of Artificial Sequence: peptide 7-26 OTHER INFORMATION: of p33ING2 (KMP1)
                                                                                                                                                                                   CORRESPONDENCE ADDRESS
                                                                                                                                 CITY: San Diego
                                                                                                                                                    STREET:
                                                                                                                                                                      ADDRESSEE:
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                                                                                                                California
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501 West Broadway
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Pred. No. 2.1e+03;
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Pred. No. 1.9e+03;
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                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 182
SOFTWARE: Patent.pm
SEQ ID NO 22
LENGTH: 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 22, Application US/09247155A
Patent No. 6312922
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, Jean-Baptiste
APPLICANT: Buclert, Aymeric
APPLICANT: Bougueleret, Lydie
APPLICANT: Bougueleret, Lydie
TITLE OF INVENTION: Complementary DNAs
FILE REFERENCE: GENSET.021A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity Matches 2; Conserv
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Query Match 57.9%; Score 11; DB 2; Best Local Similarity 33.3%; Pred. No. 3.1e+03; Matches 2; Conservative 0; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/247,155A
CURRENT FILING DATE: 1999-02-09
EARLIER APPLICATION NUMBER: 60/074,121
EARLIER FILING DATE: 1998-02-09
EARLIER FILING DATE: 1998-02-03
EARLIER FILING DATE: 1998-04-13
EARLIER APPLICATION NUMBER: 60/96,116
EARLIER APPLICATION NUMBER: 60/96,116
EARLIER FILING DATE: 1998-08-10
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INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 37 amino acida
TYPE: AMINO ACID
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                            EARLIER APPLICATION NUMBER: 60/099,273
EARLIER FILING DATE: 1998-10-04
                                                                                                   LOCATION: 1..37
OTHER INFORMATION: Von Heijne matrix
OTHER INFORMATION: score 5.9
OTHER INFORMATION: seq LSYASSALSPCLT/AP
                                                                                                                                                                                         FEATURE:
NAME/KEY: SIGNAL
                                                                                                                                                                                                                                   ORGANISM: Homo Sapiens
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-8550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: US/08/905,223
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ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: 1.37
IDENTIFICATION METHOD: Von Heijne matrix
OTHER INFORMATION: score 5.9
OTHER INFORMATION: seq LSYASSALSPCLT/AP
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CLASSIFICATION:
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LOCATION: 1..37
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33.3%;
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Pred. No. 3.1e+03;
0; Mismatches 4
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      4; Indels
                                            Length 37;
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, Jean-Baptiste
APPLICANT: Duclert, Aymeric
APPLICANT: Duclert, Aymeric
APPLICANT: Bugueleret, Lydie
TITLE OF INVENTION: Complementary DNAs
FILE REFERENCE: GENSET.021A
CURRENT APPLICATION NUMBER: US/09/903,190
CURRENT FILING DATE: 2001-07-11
PRIOR APPLICATION NUMBER: US/09/247,155A
PRIOR APPLICATION NUMBER: US/09/247,155A
PRIOR APPLICATION NUMBER: APPLICATION NUMBER: 60/074,121
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/074,121
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/081,563
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/081,563
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US-09-903-190-22
US-09-903-190-22
Sequence 22, Application US/09903190
Patent No. 6936692
Patent No. 6936692
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PRIOR FILING DATE: 1998-11-13
PRIOR FILING DATE: 1998-11-13
PRIOR FILING DATE: 1997-11-13
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/069,957
PRIOR PELICATION NUMBER: 60/074,121
PRIOR APPLICATION NUMBER: 60/074,121
PRIOR APPLICATION NUMBER: 60/081,563
PRIOR APPLICATION NUMBER: 60/081,563
PRIOR FILING DATE: 1998-04-13
PRIOR FILING DATE: 1998-04-13
PRIOR APPLICATION NUMBER: 60/096,116
PRIOR FILING DATE: 1998-04-13
PRIOR FILING DATE: 1998-04-13
PRIOR FILING DATE: 1998-04-13
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SEQ ID NO 22
LENGTH: 37
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Dumas Milne Edwards, Jean-Baptiste APPLICANT: Duclert, Aymeric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: 60/099,273 PRIOR FILING DATE: 1998-09-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: EXTENDED CDNAS FOR SECRETED PROTEINS FILE REFERENCE: 31.US3.CIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: SIGNAL LOCATION: 1..37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo Sapiens
FILING DATE: EARLIER FILING DATE: 1998-04-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22, Application US/09663600A
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score 5.9
seq LSYASSALSPCLT/AP
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33.3%;
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Pred. No. 3.1e+03;
0; Mismatches 4
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PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/096,116
PRIOR FILING DATE: EARLIER FILING DATE: 1998-08-10
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/099,273
PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-04
NUMBER OF SEQ ID NOS: 182
SOFTWARE: Patent.pm
SEQ ID NO 22
LENGTH: 37
TYPE: PRT
ORGANISM: Homo Sapiens
FEATURE:
NAME/KEY: SIGNAL
LOCATION: 1..37
OTHER INFORMATION: Won Heijne matrix
OTHER INFORMATION: seq LSYASSALSPCLT/AP
OTHER INFORMATION: seq LSYASSALSPCLT/AP
                                                                                                                                                                                  LENGTH: 40 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-812-586-40
                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/812,586
FILING DATE: 07-WAR-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 08/78
REFERENCE/DOCKET NUMBER: 08/78
REFERENCE/DOCKET NUMBER: 0575/53862-A
TELECOMPUNICATION: INFORMATION:
TELEPHONE: (212) 278-0400
TELEPAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 40 amino acids
TYPER: 40 amino acids
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US-08-812-586-40
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Query Match 57.9%; Score 11; DB 2; Best Local Similarity 33.3%; Pred. No. 3.3e+03; Matches 2; Conservative 0; Mismatches 4
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Patent No. 6048704
GENERAL INFORMATION:
APPLICANT: Martin David Tilson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 57.9%; Score 11; DB 2; Length 37; Best Local Similarity 33.3%; Pred. No. 3.1e+03; Matches 2; Conservative 0; Mismatches 4; Indels
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COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compartible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING DESCRIPTION DESCRIPTION OF THE POSITION OF 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: PURITITLE OF INVENTION: PROTITILE OF INVENTION: DISH NUMBER OF SEQUENCES: 61 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27 YASSAL 32
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VENTION: PURIFIED AND RECOMBINANT ANTIGENIC
VENTION: PROTEINS ASSOCIATED WITH ABDOMINAL AORTIC ANEURYM (AAA)
VENTION: DISEASE, AND DIAGNOSTIC AND THERAPEUTIC USES THEREOF
                                                                                           Length 40;
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Search completed: November 29, 2005, 23:04:23 Job time: 24.8636 secs

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Minimum
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Match Length
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Maximum Match 100%
Listing first 45 summaries
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1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*

6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*
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Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                      US-10-105-545-8
US-11-120-835-65
US-11-073-349-65
US-10-105-545-21
US-10-109-643-54
US-10-109-945A-2
US-10-197-945A-2
US-10-197-945A-2
US-10-197-913-619
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US-10-197-913-619
US-10-197-913-67
US-10-197-913-9-67
US-10-197-913-9-25
US-10-197-913-22
US-10-319-72-23
US-10-319-73-32
US-10-425-115-361971
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                                       67, Appl 287301, 250421, 250421, 22, Appl 122, Appl 123132, 27, Appl 120714, 361971, 361971, Appl 6611,  Appl 66111, Appl 66111, Appl 66111, Appl 66111, Appl 66111, 
                                                                                                                                                                                                                                                                                                8, Appli
65, Appl
65, Appl
21, Appl
21, Appl
66, Appl
66, Appl
2, Appli
60, App
616, Appli
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5, Appli
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45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28
11	11	11	11	11	11	11	11	11	11	11	11	11	11	11	11	11	11
57.9	57.9	57.9	57.9	57.9	57.9	57.9	57.9	57.9	57.9	57.9	57.9	57.9	57.9	57.9	57.9	57.9	57.9
55 4	55	55 4	55 4	54	53 4	52 4	52 4	51 4	50 6	50 4	50 3	49 4		49 4	49 4	48 4	45 4
US-10-425-115-317178	US-10-437-963-179375	US-10-424-599-199688	US-10-424-599-171812	US-10-856-499-933	US-10-424-599-217394	US-10-425-115-366925	US-10-218-102-329	US-10-424-599-154170	US-11-075-234-379	US-10-425-115-321893	US-09-978-360A-624	US-10-425-115-325114	US-10-425-115-321205	US-10-425-115-201880	US-10-437-963-142578	US-10-424-599-169349	US-10-425-115-354302
Sequence 317178,	Sequence 179375,	Sequence 199688,			Sequence 217394,	Sequence 366925,	Sequence 329, App	Sequence 154170,		Sequence 321893,	Sequence 624, App	Sequence 325114,	Sequence 321205,	Sequence 201880,	Sequence 142578,		

RESULT 1 US-10-105-545-8

ALIGNMENTS

Sequence 8, Application US/10105545 Publication No. US20030144479A1 GENERAL INFORMATION:

US.

CURRENT FILING DATE: 190-01-25

PRIOR REPLICATION NUMBER: US 08/752,816

PRIOR APPLICATION NUMBER: US 08/752,816

PRIOR APPLICATION NUMBER: US 07/940,654

PRIOR APPLICATION NUMBER: US 07/940,654

PRIOR PRIOR APPLICATION NUMBER: US 07/702,833

PRIOR PILING DATE: 1992-09-03

PRIOR PRIOR APPLICATION NUMBER: US 07/326,328

PRIOR PILING DATE: 1991-05-20

PRIOR PILING DATE: 198-03-21

PRIOR PILING DATE: 198-07-16

PRIOR PILING DATE: 198-07-16

PRIOR APPLICATION NUMBER: US 07/074,264

PRIOR PILING DATE: 1980-01-09

PRIOR PILING DATE: 1990-01-09

PRIOR PILING DATE: 1990-01-09

PRIOR PILING DATE: 1991-01-25

PRIOR APPLICATION NUMBER: US 07/648,303

PRIOR PILING DATE: 1991-04-15

PRIOR APPLICATION NUMBER: US 07/674,391

PRIOR APPLICATION NUMBER: US 07/574,391

PRIOR PILING DATE: 1990-08-27

S-10-105-545-8 SOFTWARE: Pac SEQ ID NO 8 SEQ TH: 17 Query Match Best Local APPLICANT: Mark, Greene I.
APPLICANT: Williams, Williams V.
APPLICANT: Weiner, David B.
APPLICANT: Cohen, Jeffery A.
APPLICANT: Kieber-Emmons, Thomas APPLICANT: Williams, Robert M.
TITLE OF INVENTION: BIOLOGICALLY ACTIVE COMPOUNDS AND
TITLE OF INVENTION: SAME Remaining Prior Application data NUMBER OF SEQ ID NOS: 32 PRIOR APPLICATION NUMBER: US 07/194,026 PRIOR FILING DATE: 1988-05-13 FILE REFERENCE: 4040/1L492US2 OTHER INFORMATION: synthetic peptide FEATURE: ORGANISM: Artificial Sequence PatentIn version 3.1 57.9%; milarity 33.3%; Conservative (Score 11; DB 4; Lo Pred. No. 3.8e+03; 0; Mismatches 4; removed • See File Wrapper or PALM Length 17; METHODS QF CONSTRUCTING AND

Matches

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US-10-120-835-65
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 65
LENGTH: 17
TYPE: PRT
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Publication No.
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Publication No. US20050214211A1
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Morrison, Karen J. M.
APPLICANT: Morrison, Robert K.
APPLICANT: Ge, Wangmao
APPLICANT: Jakobovitz, Aya
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
TITLE OF INVENTION: ENTITLED 121P2A3 USEFUL IN TREATMENT AND DETECTION OF CANCER
FILE REFERENCE: 51158-20061.00
CURRENT APPLICATION NUMBER: US/11/073,349
CURRENT FILING DATE: 2005-03-03
                                                                                                                                                                                                                                     APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US 60/286,630
PRIOR FILING DATE: 2001-04-25
PRIOR APPLICATION NUMBER: US 60/300,373
PRIOR FILING DATE: 2001-06-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Saffran, Douglas
APPLICANT: Morrison, Karen J. M.
APPLICANT: Morrison, Robert K.
APPLICANT: Ge, Wangmao
APPLICANT: Jakobovitz, Aya
APPLICANT: Jakobovitz, Aya
APPLICANT: Jakobovitz, Aya
TITLE OF INVENTION: WICLEIC ACID AND CORRESPONDING PROTEIN
TITLE OF INVENTION: ENTITLED 121P2A3 USEFUL IN TREATMENT AND DETECTION OF CANCER
FILE REFERENCE: 51158-20061.00
CURRENT APPLICATION NUMBER: US/10/120,835
CURRENT FILING DATE: 2002-09-12
CURRENT FILING DATE: 2002-09-12
                                                                                                                                                                                                                                                                             APPLICANT: Agensys, Inc.
APPLICANT: Challita-Eid
APPLICANT: Raitano, Art
APPLICANT: Faris, Mary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: US 60/282,739 PRIOR FILING DATE: 2001-04-10
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Mitchell, Steve C.
Afar, Daniel E. H.
                                                                                                                                               Saffran, Douglas
Morrison, Karen J. M.
Morrison, Robert K.
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Mitchell, Steve C.
Afar, Daniel E. H.
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Raitano, Arthur B.
Faris, Mary
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vo. US20040018189A1
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Pred. No. 3.8e+03
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: US 08/752,816
PRIOR FILLING DATE: 1996-11-21
PRIOR APPLICATION NUMBER: US 07/940,654
PRIOR FILLING DATE: 1992-09-03
PRIOR APPLICATION NUMBER: US 07/702,833
PRIOR FILLING DATE: 1991-05-20
PRIOR APPLICATION NUMBER: US 07/326,328
PRIOR APPLICATION NUMBER: US 07/326,328
PRIOR FILLING DATE: 1989-03-21
PRIOR APPLICATION NUMBER: US 07/074,264
PRIOR FILLING DATE: 1987-07-16
                                                                                                                                                      Remaining Prior Application data removed
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn version 3.1
SEQ ID NO 21
LENGTH: 18
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Matches
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 65
LENGTH: 17
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Query Match
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PRIOR APPLICATION NUMBER: US 60/282,739
PRIOR FILING DATE: 2001-04-10
PRIOR APPLICATION NUMBER: US 60/286,630
PRIOR FILING DATE: 2001-04-25
PRIOR APPLICATION NUMBER: US 60/300,373
PRIOR FILING DATE: 2001-06-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILE REFERENCE: 4040/1L492US2
CURRENT APPLICATION NUMBER: US/10/105,545
CURRENT FILING DATE: 2002-09-06
                                                                                                                                                                                                                                                                                                                    PRIOR FILING DATE: 1990-01-09
PRIOR APPLICATION NUMBER: US 07/648,303
PRIOR APPLICATION NUMBER: US 07/685,881
PRIOR APPLICATION NUMBER: US 07/685,881
PRIOR FILING DATE: 1991-04-15
PRIOR APPLICATION NUMBER: US 07/574,391
PRIOR FILING DATE: 1990-08-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Kieber-Emmons, Thomas
APPLICANT: Williams, Robert M.
TITLE OF INVENTION: BIOLOGICALLY ACTIVE COMPOUNDS AND METHODS OF CONSTRUCTING AND USING TITLE OF INVENTION: SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Williams, Willia APPLICANT: Weiner, David B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: US/10/120,835
                                                                                                                                                                                                                                                                     PRIOR FILING DATE: 1988-05-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Mark, Greene I
                                                                                    TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
                                                                    OTHER INFORMATION: synthetic peptide
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2; Conser
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No. US20030144479A1
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    57.9%; Score 11;
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Pred. No.
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    See File Wrapper or PALM

    DB 4;
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  Length 18;
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; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-120-835-66
                                                                                                                                              FILE REFERENCE: 51158-20061.00
CURRENT APPLICATION NUMBER: US/10/120,835
CURRENT FILING DATE: 2002-09-12
PRIOR APPLICATION NUMBER: US 60/282,739
PRIOR FILING DATE: 2001-04-10
PRIOR APPLICATION NUMBER: US 60/286,630
PRIOR APPLICATION NUMBER: US 60/286,630
PRIOR APPLICATION NUMBER: US 60/300,373
PRIOR APPLICATION NUMBER: US 60/300,373
PRIOR APPLICATION NUMBER: US 60/300,373
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APPLICANT: Hartzell, William
APPLICANT: Hartzell, William
APPLICANT: Hartzell, William
APPLICANT: Hartzell, William
APPLICATION NUMETHONS AND COMPOSITIONS FOR PREVENTING AND TREATING MICROBIAL:
FILE REFERENCE: B00801.70281.US
CURRENT APPLICATION NUMBER: US/10/409,643
CURRENT FILING DATE: 2003-04-08
PRIOR FILING DATE: 2002-04-08
PRIOR FILING DATE: 2002-04-08
NUMBER OF SEQ ID NOS: 55
SOFTWARE: Patentin version 3.1
SEQ ID NO 54
LENGTH: 18
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Matches 2; Conserv
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Best Local Similarity 33.3%;
Matches 2; Conservative
                                                               SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 66 LENGTH: 19
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
TITLE OF INVENTION: ENTITLED 121P2A3 USEFUL IN TREATMENT !
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                                                                                                                                NUMBER OF SEQ ID NOS: 82
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Hubert, Rene S.
Mitchell, Steve C.
Afar, Daniel E. H.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Saffran, Douglas
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0; Mismatches
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Pred. No. 4e+03;
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APPLICANT: Jakobovitz, Aya
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
TITLE OF INVENTION: ENTITLED 121P2A3 USEFUL IN TREATMENT AND
FILE REFERENCE: 51158-20061.00
CURRENT APPLICATION NUMBER: US/11/073,349
CURRENT FILING DATE: 2005-03-03
PRIOR APPLICATION NUMBER: US/10/120,835
PRIOR APPLICATION NUMBER: US/022,739
PRIOR FILING DATE: 2002-09-12
PRIOR FILING DATE: 2001-04-10
PRIOR APPLICATION NUMBER: US 60/282,739
PRIOR APPLICATION NUMBER: US 60/286,630
PRIOR APPLICATION NUMBER: US 60/286,630
PRIOR APPLICATION NUMBER: US 60/286,630
PRIOR APPLICATION NUMBER: US 60/286,630
PRIOR APPLICATION NUMBER: US 60/286,630
PRIOR APPLICATION NUMBER: US 60/286,630
PRIOR APPLICATION NUMBER: US 60/300,373
PRIOR APPLICATION NUMBER: US 60/300,373
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Best Local
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APPLICANT:
APPLICANT:
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Best Local Similarity
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APPLICANT:
APPLICANT:
APPLICANT: Masuda, Esteban
APPLICANT: Kinsella, Todd M
APPLICANT: Warner, Justin E
APPLICANT: Warner, Justin E
APPLICANT: Bennett, Mark K
APPLICANT: Bennett, Mark K
APPLICANT: Anderson, David C
TITLE OF INVENTION: Methods of Identifying Compounds that Modulate IL-4 Receptor-Med.
TITLE OF INVENTION: Synthesis Utilizing a Chloride Intracellular Channel 1 Protein
FILE REFERENCE: RIGL-013/00US
FILE REPERENCE: RIGL-013/00US
CURRENT APPLICATION NUMBER: US/10/197,945A
CURRENT FILING DATE: 2002-10-15
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION:
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Mitchell, Steve C.
Afar, Daniel E. H.
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Morrison, Karen J. M.
Morrison, Robert K.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ge, Wangmao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Raitano, Arthur B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Challita-Eid, Pia M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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33.3%;
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33.3%;
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Pred. No. 4.1e+03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 11; DB 6;
Pred. No. 4.1e+03;
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RESULT 10
US-10-776-013-616
; Sequence 616, Application US/10776013
; Publication No. US20040226056A1
; GENERAL INFORMATION:
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                                                                                                                                                                                                             Query Match
Best Local Similarity
""" Ahes 2; Conserve
                                                                                                                                                                                                                                                                                                                 ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-776-013-609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/10/776,013
CURRENT FILING DATE: 2004-02-09
PRIOR APPLICATION NUMBER: 09/948904
PRIOR FILING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: 09/466139
PRIOR APPLICATION NUMBER: 09/11534
PRIOR PILING DATE: 1999-12-21
PRIOR APPLICATION NUMBER: 60/124120
PRIOR FILING DATE: 1998-12-22
PRIOR FILING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: 60/141243
PRIOR APPLICATION NUMBER: 60/141243
PRIOR FILING DATE: 1999-03-12
PRIOR FILING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: 60/14079
PRIOR APPLICATION NUMBER: 60/240790
PRIOR APPLICATION NUMBER: 60/240790
PRIOR APPLICATION NUMBER: 60/240790
PRIOR APPLICATION NUMBER: 60/240790
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/240790
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/240790
PRIOR FILING DATE: 2000-10-17
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US-10-776-013-609
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US-10-197-945A-2
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Best Local Similarity 33.3
Matches 2; Conservative
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LENGTH: 20
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SEQ ID NO 609
LENGTH: 20
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SOFTWARE: PatentIn version
                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 10/194967
PRIOR FILING DATE: 2002-07-15
PRIOR APPLICATION NUMBER: 60/304775
PRIOR FILING DATE: 2001-07-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING NEUROLOGICAL DISORDERS AND TITLE OF INVENTION: DISEASES FILE REFERENCE: 1600.24
                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 695
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Bartel, Paul
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Pred. No. 4.3e+03
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pred. No. 4.3e+03;
0; Mismatches 4
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                                                                                                                                                                                                                                                                        Length 20;
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Query Match
Best Local Similarity
Watches 2; Conserve
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US-10-868-270-5
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; ORGANISM: Homo mapiens
US-10-776-013-616
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SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 5
LENGTH: 20
TYPE: PRT
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SEQ ID NO 616
LENGTH: 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
Query Match
                                                                                                                                                                                                                                                                                             APPLICANT: Harris, Curtis C
APPLICANT: Nagashima, Makoto
APPLICANT: Nagashima, Makoto
APPLICANT: Government of United States as represented by the Secretary of the
APPLICANT: Department of Health and Human Services
TITLE OF INVENTION: New Tumor Suppressor Gene P33ING2
FILE REFERENCE: 015280-376100US
CURRENT APPLICATION NUMBER: US/10/868,270
CURRENT FILING DATE: 2004-06-14
PRIOR APPLICATION NUMBER: US/09/513,365
PRIOR APPLICATION NUMBER: US/09/513,365
PRIOR APPLICATION NUMBER: US/09/513,365
PRIOR APPLICATION NUMBER: US/09/513,365
PRIOR APPLICATION NUMBER: US/09/513,365
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CURRENT FILING DATE: 2004-02-09
PRIOR APPLICATION NUMBER: 09/948904
PRIOR FILING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: 09/466139
PRIOR FILING DATE: 1999-12-21
PRIOR FILING DATE: 1999-12-21
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APPLICANT: Heichman, Karen
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING NEUROLOGICAL DISORDERS AND
TITLE OF INVENTION: DISEASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR FILING DATE: 2001-07-13
NUMBER OF SEQ ID NOS: 695
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PRIOR APPLICATION NUMBER: 60/304775
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PRIOR FILING DATE: 1999-06-30
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PRIOR FILING DATE: 1998-12-22
PRIOR APPLICATION NUMBER: 60/124120
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                                                                          OTHER INFORMATION: OTHER INFORMATION:
                                                                                                                                                     ORGANISM: Artificial Sequence
                                                                                                                             FEATURE:
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                                                                       Description of Artificial Sequence: peptide 7-26 of p33ING2 (KMP1)
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33.3%;
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Score 11;
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Pred. No. 4.3e+03;
0; Mismatches 4
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Length 20;
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Length 28;

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Gaps

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TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
TITLE OF INVENTION: ENTITLED 121P2A3 USEFUL IN TREATMENT AND
FILE REFERENCE: 51158-20061.00
CURRENT APPLICATION NUMBER: US/10/120,835
CURRENT FILING DATE: 2002-09-12
PRIOR APPLICATION NUMBER: US 60/282,739
PRIOR APPLICATION NUMBER: US 60/282,739
PRIOR FILING DATE: 2001-04-10
PRIOR FILING DATE: 2001-04-25
PRIOR APPLICATION NUMBER: US 60/286,630
PRIOR FILING DATE: 2001-04-25
PRIOR APPLICATION NUMBER: US 60/300,373
PRIOR APPLICATION NUMBER: US 60/300,373
PRIOR PILING DATE: 2001-06-22
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US-10-120-835-67
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APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT APPLICATION NUMBER: US/10/424,599
SURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 275349
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Publication No. US20040018189A1
GENERAL INFORMATION:
APPLICANT: Agensys, Inc.
APPLICANT: Challita-Eid, Pia
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Best Local Similarity 33.3%;
Matches 2; Conservative
           NUMBER OF SEQ ID NOS: 82
SOFTWARE: FABTSEQ for WiseQ ID NO 67
LENGTH: 28
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APPLICANT:
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ORGANISM: Glycine max
FEATURE:
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Mitchell, Steve C.
Afar, Daniel E. H.
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Faris, Mary
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Saffran, Douglas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Challita-Eid, Pia M. Raitano, Arthur B.
                                                                                                                                                                                                                                                                                                                                                       Jakobovitz, Aya
                                                                                                                                                                                                                                                                                                                                                                          Ge, Wangmao
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                                                               for Windows Version 4.0
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0; Mismatches 4;
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Pred. No. 5.4e
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TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
TITLE OF INVENTION: ENTITLED 121P2A3 USEFUL IN TREATMENT AND
FILE REFERENCE: 51158-20061.00
CURRENT APPLICATION NUMBER: US/11/073,349
CURRENT FILLING DATE: 2005-03-03
PRIOR APPLICATION NUMBER: US/10/120,835
PRIOR APPLICATION NUMBER: US/00/20,835
PRIOR FILLING DATE: 2002-09-12
PRIOR FILLING DATE: 2001-04-10
PRIOR FILLING DATE: 2001-04-10
PRIOR APPLICATION NUMBER: US 60/286,630
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Best Local Similarity
Matches 2; Conserve
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US-10-425-115-287301
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Publication No. US20050214211A1
GENERAL INFORMATION:
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Best Local Similarity 33.1
Matches 2; Conservative
                Sequence 287301, Application US/10425115
Publication No. US20040214272A1
Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Cao, Yinua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(5322)B
FULE REFERENCE: 38-21(5322)B
CURRENT APPLICATION NUMBER: US/10/425,115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 82
SOPTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 67
LENGTH: 28
TYPE: PRT
ORGANISM: Homo Sapiens
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APPLICANT: Challita-Ei
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CURRENT FILING DATE:
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Morrison, Robert K.
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33.3%;
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Pred. No. 5.6e+03;
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Pred. No. 5.
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Length 28 Indels

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Gaps

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; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 287301
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_25114C.1.pep
US-10-425-115-287301

Query Match
Best Local Similarity 33.3%; Pred. No. 5.9e+03;
Matches 2; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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5earch completed: November 29, 2005, 23:10:29
Job time: 78.9545 secs
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Listing first 45 summaries
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seq length: 2000000000
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1: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
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Match Length
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12.124 Million cell updates/sec
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          GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.
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                           US-10-510-386-114
US-11-144-248-40
US-11-144-248-42
US-10-507-662-40
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US-10-506-501-151
US-11-144-248-48
US-11-144-248-52
US-11-054-515-1932
US-11-054-515-1932
US-11-054-515-2054
US-11-054-515-164
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US-11-054-515-164
US-11-054-515-164
US-11-054-515-164
US-11-054-515-1881
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Sequence 114, App Sequence 40, Appl Sequence 40, Appl Sequence 11, Appl Sequence 151, App Sequence 152, Appl Sequence 157, App Sequence 1932, Appl Sequence 1932, Appl Sequence 1934, App Sequence 82, Appl Sequence 82, Appl Sequence 164, App Sequence 261, App Sequence 275, Ap Sequence 280, Appl Sequence 1881, App Sequence 1846, App Sequence 1446, App Sequence 1446, App Sequence 1174, Ap Sequence 1174, Ap Sequence 1310, App Sequen
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US-10-510-386-114
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11 57.9 316 10S-10-34-34-45-45 11 57.9 348 7 US-11-137-465-45 11 57.9 448 7 US-11-137-465-45 11 57.9 708 1 US-10-921-234-917 11 57.9 708 1 US-10-921-234-917 11 57.9 775 1 US-10-997-697-5 1 US-10-997-697-3 1 US-10-997-697-3 1 US-10-997-697-3 1 US-10-997-697-8 1 US-10-997-697-8 1 US-10-997-697-1 1 1 52.6 29 1 US-10-997-697-1 1 1 52.6 29 1 US-10-997-697-1 1 1 52.6 29 1 US-10-997-697-1 1 1 52.6 29 1 US-10-997-697-1 1 1 52.6 29 1 US-10-997-697-1 1 1 52.6 29 1 US-10-997-697-1 1 1 52.6 29 1 US-10-997-697-1 1 1 52.6 29 1 US-10-997-697-1 1 1 52.6 29 1 US-10-997-697-1 1 1 52.6 62 1 US-10-997-697-1 1 1 52.6 100 7 US-11-44-248-1 0 52.6 100 7 US-11-144-248-1 0 52.6 100 3 1 US-10-93-656-2074 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	45	44	43	42	41	40	39	38	37	36	35	υ 4	33	32	31	30	29	28	27	26
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Query Match
Best Local Similarity
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US-11-144-248-40
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SOFTWARE: Patentin version 3.3
SEQ ID NO 114
LENGTH: 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 114, Application US/10510386 Publication No. US20050244922A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Andersen, Jens Tonne
APPLICANT: Clausen, Ib Groth
APPLICANT: Jorgensen, Steen Troels
APPLICANT: Jorgensen, Steen Troels
APPLICANT: Rasmussen, Michael Dolberg
APPLICANT: Rasmussen, Michael Dolberg
FILE OF INVENTION: Improved Bacillus Host Cell
FILE REFERENCE: 10294.204-US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/10/510,386
CURRENT FILING DATE: 2004-10-04
                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Bacillus licheniformis
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Pred. No. 1.1e+02;
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; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 40
; LENGTH: 96
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-144-248-40
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US-11-144-248-42
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Best Local Similarity 33.2
Thes 2; Conservative
                                                                                                                                                                                                                                                     Sequence 40, Application US/10507662 Publication No. US20050255102A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 42
LENGTH: 96
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SEQ ID NO 40
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                                                  APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA TITLE OF INVENTION: ANTI-ALPHA-V BETA-6 ANTIBODIES FILE REFERENCE: A136PCT CURRENT APPLICATION NUMBER: US/10/507,662 CURRENT FILING DATE: 2004-09-13 PRIOR APPLICATION NUMBER: 60/364,991 PRIOR APPLICATION NUMBER: 60/364,991 PRIOR PILING DATE: 2002-03-13 PRIOR APPLICATION NUMBER: 60/364,291 PRIOR PILING DATE: 2002-03-13 PRIOR FILING DATE: 2002-03-13 PRIOR FILING DATE: 2002-11-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILE REFERENCE: ABX-PF2
CURRENT APPLICATION NUMBER: US/11/144,248
CURRENT FILING DATE: 2005-06-02
PRIOR APPLICATION NUMBER: US/10/038,591
PRIOR FILING DATE: 2002-01-04
PRIOR APPLICATION NUMBER: 60/259,927
PRIOR FILING DATE: 2001-01-05
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APPLICANT: Gallo, Michael
TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Cohen, Bruce D. APPLICANT: Beebe, Jean
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PRIOR FILING DATE: 2001-01-05
NUMBER OF SEQ ID NOS: 60
                  NUMBER OF SEQ ID NOS: 64
SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                APPLICANT: BIOGEN, APPLICANT: THE REC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Homo sapiens
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les 2; Conservarive
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Pred. No. 1.2e+02;
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Pred. No. 1.2e+02;
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CURRENT APPLICATION NUMBER: US/10/507,662
CURRENT FILING DATE: 2004-09-13
PRIOR APPLICATION NUMBER: 60/364,991
PRIOR FILING DATE: 2002-03-13
PRIOR APPLICATION NUMBER: 60/426,286
PRIOR FILING DATE: 2002-11-13
NUMBER OF SEQ ID NOS: 64
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 41
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-507-662-40
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Publication No. US20050255102A1
GENERAL INFORMATION:
APPLICANT: BIOGEN, INC.
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Best Local
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                                                                                                                                                                    PRIOR APPLICATION NUMBER: US/10/621,363
PRIOR FILING DATE: 2003-07-18
PRIOR APPLICATION NUMBER: 09/969,730
PRIOR FILING DATE: 2001-10-06
PRIOR APPLICATION NUMBER: 09/774,639
PRIOR FILING DATE: 2001-02-01
                                                                                                                                                                                                                                                                                     FILE REFERENCE: PZ013P2C1
CURRENT APPLICATION NUMBER: US/10/986,501
CURRENT FILING DATE: 2004-11-12
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APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
TITLE OF INVENTION: ANTI-ALPHA-V BETA-6 ANTIBODIES
FILE REFERENCE: A136PCT
                                                                                                                              PRIOR FILING DATE: 2000-10-06
                                                                                                                                                  PRIOR FILING DATE: 2001-02-01
PRIOR APPLICATION NUMBER: 60/238,291
                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: 90 Human Secreted Proteins
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TYPE: PRT
ORGANISM: Homo sapiens
                                   APPLICATION NUMBER: PCT/US98/16235
FILING DATE: 1998-08-04
APPLICATION NUMBER: 60/056,371
                                                                                           APPLICATION NUMBER: 09/244,112
FILING DATE: 1999-02-04
APPLICATION NUMBER: 60/056,732
                   FILING DATE: 1997-08-19
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Pred. No.
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1.3e+02;
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US-11-144-248-48
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 151
LENGTH: 108
TYPE: PRT
ORGANISM: Homo sapiens
                                                      GENERAL INFORMATION:
APPLICANT: Cohen, Bruce D.
APPLICANT: Heebe, Jean
APPLICANT: Miller, Penelope E.
APPLICANT: Miller, Penelope E.
APPLICANT: Moyer, James D.
APPLICANT: Corvalan, Jose R.
APPLICANT: Gallo, Michael
TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR
FILE REPERENCE: ABX-PF2
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Best Local Similarity
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Best Local Similarity
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APPLICANT: Moyer, James D.
APPLICANT: Corvalan, Jose R.
APPLICANT: Gollo, Michael
TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR FILE REFERENCE: ABX-PF2
CURRENT APPLICATION NUMBER: US/11/144,248
CURRENT FILING DATE: 2005-06-02
PRIOR APPLICATION NUMBER: US/10/038,591
PRIOR FILING DATE: 2002-01-04
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PRIOR APPLICATION NUMBER: 60/056,364
PRIOR FILING DATE: 1997-08-19
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NUMBER OF SEQ ID NOS: 60
SOFTWARE: Patentin Ver. 2.1
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CURRENT APPLICATION NUMBER: US/11/144,248
CURRENT FILING DATE: 2005-06-02
PRIOR APPLICATION NUMBER: US/10/038,591
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Homo sapiens
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33.3%;
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Pred. No. 1.3e+02;
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Pred. No. 2.1e+02;
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Best Local Similarity
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RESULT 10
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US-11-054-515-1577
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PRIOR FILING DATE: 2004-02-11
PRIOR APPLICATION NUMBER: 60/580,347
PRIOR APPLICATION NUMBER: 60/580,347
PRIOR FILING DATE: 2004-06-18
PRIOR APPLICATION NUMBER: 10/293,418
PRIOR FILING DATE: 2002-11-14
PRIOR APPLICATION NUMBER: 60/31,469
PRIOR FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: 60/340,817
PRIOR FILING DATE: 2001-12-19
PRIOR FILING DATE: 2001-12-19
PRIOR FILING DATE: 2001-12-19
                                                                                                                                                                                                                                                    PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 3247
LENGTH: 241
TYPE: PRT
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SEQ ID NO 52
LENGTH: 236
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                                                                                                                                                                        Query Match
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TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REFERENCE: PF523P3
CURRENT APPLICATION NUMBER: US/11/054,515
CURRENT FILING DATE: 2005-02-10
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PRIOR APPLICATION NUMBER: 60/259,927
PRIOR FILING DATE: 2001-01-05
NUMBER OF SEQ ID NOS: 60
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PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/276,248
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                                                         182 YAASSL 187
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Pred. No. 2.1e+02;
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Pred. No. 2.2e+02;
0; Mismatches 4
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US-11-054-515-1932

Sequence 1932, Application US/11054515 Publication No. US2005025532A1 GENERAL INFORMATION:

APPLICANT: Ruben et al.

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RESULT 11
US-11-054-515-2054
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US-11-054-515-1932
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PRIOR FILLING DATE: 2004-06-18
PRIOR PELICATION NUMBER: 10/293,418
PRIOR FILLING DATE: 2002-11-14
PRIOR APPLICATION NUMBER: 60/331,469
PRIOR FILLING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: 60/3310,817
PRIOR APPLICATION NUMBER: 60/340,817
PRIOR APPLICATION NUMBER: 60/880,748
PRIOR APPLICATION NUMBER: 09/880,748
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PRIOR FILING DATE: 2002-11-14
PRIOR PELICATION NUMBER: 60/331,469
PRIOR PELLORITON NUMBER: 60/331,469
PRIOR APPLICATION NUMBER: 60/340,817
PRIOR FILING DATE: 2001-12-19
PRIOR PELICATION NUMBER: 09/880,748
PRIOR FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/293,499
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Best Local
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SEQ ID NO 1932
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PRIOR FILING DATE: 2004-02-11
PRIOR APPLICATION NUMBER: 60/580,347
PRIOR FILING DATE: 2004-06-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILE REFERENCE: PF523P3
CURRENT APPLICATION NUMBER: US/11/054,515
CURRENT FILING DATE: 2005-02-10
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CURRENT FILING DATE: 2005-02-10
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TYPE: PRT
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                                           OR FILING DATE: 2001-05-25

RAPPLICATION NUMBER: 60/277,379

OR FILING DATE: 2001-03-21

OR APPLICATION NUMBER: 60/276,248

OR FILING DATE: 2001-03-16

OR APPLICATION NUMBER: 60/240,816

OR FILING DATE: 2000-10-17
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Application data removed - NOS: 3247
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Pred. No. 2.2e+02;
0; Mismatches 4
                     See File Wrapper or
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; SEQ ID NO 2054
; LENGTH: 241
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-2054
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US-11-054-515-82
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PRIOR FILING DATE: 2004-06-18
PRIOR APPLICATION NUMBER: 10/293,418
PRIOR FILING DATE: 2002-11-14
PRIOR APPLICATION NUMBER: 60/331,469
PRIOR APPLICATION NUMBER: 60/340,817
PRIOR APPLICATION NUMBER: 60/340,817
Sequence 82, Application US/11054515
Publication No. US20050255532A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind
FILE REFERENCE: PF523P3
CURRENT APPLICATION NUMBER: US/11/054,515
CURRENT FILING DATE: 2005-02-10
PRIOR APPLICATION NUMBER: 60/543,296
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Best Local Similarity 33.3
Matches 2; Conservative
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Publication No. US20050255532A1
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CURRENT FILING DATE: 2005-02-10
PRIOR APPLICATION NUMBER: 60/543,296
PRIOR FILING DATE: 2004-02-11
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TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
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TYPE: PRT
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FILING DATE: 2001-03-21
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APPLICATION NUMBER: 09/880,748
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33.3%;
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Pred. No. 2.2e
0; Mismatches
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Pred. No. 2.2e+02;
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2.2e+02;
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; SEQ ID NO 82
; LENGTH: 244
TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-82
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Remaining Prior Application data removed
NUMBER OF SEQ ID NOS: 3247
SEQ ID NO 164
LENGTH: 244
TYPE: PRT
ORGANISM: Homo sapiens
US-11-054-515-164
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PRIOR FILING DATE: 2001-03-21
PRIOR PPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
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CURRENT APPLICATION NUMBER: US/11/054,515

CURRENT FILING DATE: 2005-02-10

PRIOR APPLICATION NUMBER: 60/543,296

PRIOR FILING DATE: 2004-02-11

PRIOR APPLICATION NUMBER: 60/580,347
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Remaining Prior Application data removed - See File Wrapper or PALM NUMBER OF SEQ ID NOS: 3247
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TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
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PRIOR FILING DATE: 2001-11-16
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OR FILING DATE: 2001-12-19
OR APPLICATION NUMBER: 09/880,748
OR FILING DATE: 2001-06-15
OR APPLICATION NUMBER: 60/293,499
OR FILING DATE: 2001-05-25
OR FILING DATE: 2001-05-25
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FILING DATE: 2002-11-14
APPLICATION NUMBER: 60/331,469
FILING DATE: 2001-11-16
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APPLICATION NUMBER: 60/580,347
FILING DATE: 2004-06-18
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o. US20050255532A1
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Search completed: November 29, 2005, 23:04:39
Job time: 3.75 secs

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NUMBER OF SEQ ID NOS: 3247
SEQ ID NO 261
LENGTH: 244
TYPE: PRT
ORGANISM: Homo sapiens
US-11-054-515-261
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US-11-054-515-261
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Best Local Similarity
Matches 2; Conserv
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                                                                          Matches
                                                                                                              Query Match
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PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/240,816
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PRIOR APPLICATION NUMBER: 10/293,418
PRIOR FILING DATE: 2002-11-14
PRIOR APPLICATION NUMBER: 60/331,469
PRIOR FILING DATE: 2001-11-16
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PRIOR APPLICATION NUMBER: 60/340,817
PRIOR FILING DATE: 2001-12-19
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nes 2; Conserv
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185 YAASTL 190
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